site; cloning; att; ss.

Recombination

Unidentified

JS6171861-B1

09-JAN-2001

(first entry)

12-APR-2001

Recombination site attR3.

us-10-055-001a-11.rng

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a gene or partial gene, using recombinatorial cloning. The method incubates nucleic acids comprising the expression signal and the gene/ partial gene in the presence of a recombination protein under conditions sufficient to cause recombination and therefore appose the expression signal and the gene or partial gene. The methods are useful for apposing an expression signal and a gene or partial gene using recombinatorial cloning. The methods are also or partial gene using recombinatorial cloning. The methods are also seful for changing vectors, constructing genes for fusion proteins, changing copy number, changing replicons, at one and a loxy site at the other end), genomic DNAs, and cDNAs. The methods are highly specific, rapid, and less labour intensive than prior art methods. The present sequence is a recombination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a method for apposing an expression signal and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Methods for apposing nucleic acids comprising an expression signal an a gena/partial gene, using recombinatorial cloning by incubating the nucleic acids in the presence of a recombination protein under conditions for recombination.
                                                                                                                                                                                                                                                         Recombination site; copy number; replicon; recombinatorial cloning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 22; Length 25; 100.0%; Pred. No. 0.11;
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25
                  GTTCAGCTTTCTTGTACAAAGTTGG 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombination cloning
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95US-0486139.
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                                                                                                                                                                                         01-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (INVI-) INVITROGEN CORP.
                                                                                                                    AAD14444 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brasch MA;
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                               attP2,P3; ds
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                                                                                                                                                       AAD14444;
                                                                                                       AAD14444
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In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host

(LIFE-) LIFE TECHNOLOGIES INC.

Brasch MA;

Hartley JL,

WPI; 2001-136877/14

95US-0486139.

98US-0005476

12-JAN-1998; 07-JUN-1996; Claim 25; Column 46; 73pp; English

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The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors each comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture, and selecting for a host comprising the chimeric nucleic acid molecule, and selecting against a host comprising the vectors comprising the second vector; to clone the nucleic acid. The present sequence is a recombinantion site, which may be used in the method of the present
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nes 25; Conserv
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Gaps

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Indels

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0; Mismatches

25; Conservative

Matches

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Best Local Similarity

GITCAGCITICITGIACAAAGITGG 25 Gricagerirerieracaaagires 25

AAF55745 standard; DNA; 25 BP

AAF55745;

AAF55745 ID AAF5 XX AC AAF5 RESULT 5

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The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors each comprising at lesst one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid melecule comprising the nucleic acid of interest; contacting hosts with the mixture; and selecting for a host comprising the chimeric nucleic acid mixture, and selecting for a host comprising the chimeric nucleic acid the second vector; to clone the nucleic acid. The present sequence is a recombinantion site, which may be used in the method of the present
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                                                                                                                                                                                                                                                                                                           In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Escherichia coli core region recombinant site attR3 SEQ ID NO:11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAC87876 standard; DNA; 25 BP.
                                                                                                                           (LIFE-) LIFE TECHNOLOGIES INC.
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95US-0486139.
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nes 25; Conservative
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07-JUN-1995;
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                                 07-JUN-1996;
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                                                                                                                                                                                       Hartley JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention
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Matches
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The present invention describes an isolated nucleic acid molecule (I) comprising a first nucleic acid sequence having a defined sequence (AAC8986 to AAC87881, sequences complementary to AAC87881, or an RNA sequence corresponding to AAC87881. Also described are: (1) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site to avoids hairpin formation, the recombination site being an att or lox site; (2) an isolated nucleic acid molecule (III) comprising a first att recombination site comprising a mutation that comprising a first att recombination site comprising a mutation that above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids; and (4) cells comprising the above mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining engineered recombination in vitro or in vivo makes the methods for DNA or RNA subcloning, highly specific, rapid, and ; 0 Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank selectable marker and comprise a core region having an engineered Gaps Escherichia coli core region recombinant site attP2, P3 SEQ ID NO:16. selectable marker and comprise a core region having an engineered . 0 100.0%; Score 25; DB 22; Length 25; 100.0%; Pred. No. 0.11; 0; Indels Core region, recombination site, cloning, chimeric DNA; characteristic, mutation, att site; lox site, ss. Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other; Mismatches 1 GITCAGCITICITGIACAAGTIGG 25 GTTCAGCTTTCTTGTACAAAGTTGG 25 Claim 1; Column 18; 73pp; English ; 0 BP. (LIFE-) LIFE TECHNOLOGIES INC. 96US-0663002. 98US-0005476. 95US-0486139. 99US-0233493 AAC87881 standard; DNA; 25 (first entry) Conservative Brasch MA, Hartley JL; Query Match Best Local Similarity Thes 25; Conserve WPI; 2001-049004/06. Escherichia coli. 20-JAN-1999; 12-JAN-1998; 07-JUN-1995; 17-JUN-1996; 02-MAR-2001 US6143557-A. 07-NOV-2000 AAC87881; mutation RESULT 임 à

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Gaps

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The present invention describes an isolated nucleic acid molecule (I)

Claim 1; Column 18; 73pp; English

mutation

comprising a first nucleic acid sequence having a defined sequence comprising a first nucleic acid sequence complementary to AAC87866 to AAC87881.

Or an RNA sequence corresponding to AAC8786 to AAC87881. Also described are: (1) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site to avoids hairpin formation, the recombination site being an att or lox site; (2) an isolated nucleic acid molecule (III) comprising a first att recombination site comprising a first att recombination site comprising a first att recombination site comprising a mutation that above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids in (IV). The nucleic acids are used in entioned nucleic acids or (IV). The nucleic acids are used in consinering a core region of a given recombination site to provide mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining engineered recombination in vitro or in vivo makes the methods for DNA or RNA subcloning, highly specific, rapid, and ess labour intensive. 

Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

0; Score 25; DB 22; Length 25; Pred. No. 0.11; 0; Mismatches 0; Indels 1 GITCAGCITICITGIACAAGTIGG 25 Query Match
Best Local Similarity 100.0%;
Matches 25; Conservative 0 qq

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Gaps

Gricagcrircriciacaadried 25

AAS14786 standard; DNA; 25

27-FEB-2002 (first entry) AAS14786;

Lambda phage Int recombinase site core region DNA sequence attR3.

Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine; syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour; recombinase; tumour-specific promoter; hypoxic response element; HRE; ss; tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer; cytostatic; gene therapy; Int recombinase site core region; attR3; excisive recombination. 

Bacteriophage lambda.

WO200174861-A2.

11-0CT-2001

30-MAR-2001; 2001WO-US10250.

31-MAR-2000; 2000US-193977P.

Murphy S, Bateman A; Harrington K, Vile RG,

(MAYO-) MAYO FOUND MEDICAL EDUCATION & RES

WPI; 2001-656985/75.

Recombinant nucleic acid vector for reducing tumour size, has expression cassette comprises a promoter linked to nucleic acid sequence encoding a syncytium-inducing polypeptide and flanked on either side by recombinase

Disclosure; Page 42; 84pp; English.

The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli.

(b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a eukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and

The invention relates to a recombinant nucleic acid vector comprising a first expression cassette, comprising a first promoter operably linked to a nucleic acid acquence encoding a syncytum-inducing polypeptide (such as a fusogenic membrane glycoprotein) and flanked on either side by a sequence recognised by a recombinase, and/or a second expression cassette

comprising a tumour-specific promoter operably linked to a nucleic acid sequence encoding a recombinase. The nucleic acid of the first expression cassette may be linked to a hypoxic response element (HRE), the second expression cassette may contain a promoter linked to a nucleic acid encoding a cytokine, and a third cassette may contain a tumour specific promoter linked to the nucleic acid encoding the recombinase. The tumour specific promoter is, for example, a carcinoembryonic antigen (CEA) promoter or a tyrosinase promoter and the recombinase is, for example, or recombinase or FLP recombinase The invention is useful for reducing tumour size by administering the compositions as retroviral vectors, or in a cell containing the vector, to an individual in need of treatment for a disease caused by malignant cells. This sequence represents an Int recombinase site core region attR3, required for excisive recombination. ô New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large Gaps Chimeric nucleic acid construct, recombinational cloning; silencing; recombination site; double stranded RNA; plant; ss. ٠, 100.0%; Score 25; DB 23; Length 25; 100.0%; Pred. No. 0.11; 0; Indels Core sequence of recombination site attR3 SEQ ID NO:6. Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other; 0; Mismatches (CSIR ) COMMONWEALTH SCI & IND RES ORG. ö 1 GTTCAGCTTTCTTGTACAAGTTGG 25 GTTCAGCTTTCTTGTACAAAGTTGG 25 Disclosure; Page 15; 104pp; English. Helliwell amounts of double-stranded RNA BP Conservative Conservative 24-JAN-2002; 2002WO-AU00073. 26-JAN-2001; 2001US-264067P. 29-NOV-2001; 2001US-333743P. ABQ82123 standard; DNA; 25 (first entry) Waterhouse P, WPI; 2002-682669/73. Best Local Similarity WO200259294-A1. 25; 11-DEC-2002 01-AUG-2002. Synthetic. Wesley S, ABQ82123; Query Match Matches ABQ82123 55555555555555**X**8 ð d

the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used to conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents the core sequence of recombination site attBl which is given in the exemplification of the present invention.

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Gaps

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0; Indels

0; Mismatches

Best Local Similarity 100. Matches 25; Conservative

Query Match

1 GITCAGCITTCTIGIACAAGTIGG 25 Gricagerirerieracaaaginge 25

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Gaps

Recombination site related oligonucleotide SEQ ID NO:51.

(first entry)

29-MAY-2003

ACC44660;

BP.

ACC44660 standard; DNA; 25

RESULT 12

ACC44660

100.0%; Score 25; DB 24; Length 25; 100.0%; Pred. No. 0.11;

Seguence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

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the third and fourth recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the
                                                                                                                    phenotypic expression of nucleic acids. The present sequence represents the core sequence of recombination site attBl which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ss.
 The first and second recombination sites,
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Core sequence of recombination site attP2, P3 SEQ ID NO:11.
                                                                                                                                                                            Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
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29-NOV-2001; 2001US-333743P.
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 preferably are identical.
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The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (I) a platform artificial chromosome expression system (ACes) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (M1) is useful for introducing a heterologous nucleic acid into a platform artificial artificial chromosome, preferably an ACes. (II) is useful for transgenic animal (e.g. a fish, insect, reptile, amphibian, arachmid, or
                                                                                                                                         att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; PCR primer; ss.
                                                                                                                    Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
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                                                                                                                                                                                                                                                                                                                                                                                                                             Fleming
                                                                                                                                                                                                                                                                                                                                                                                                                               Leung J,
                                                                                                                                                                                                                                                                                                                                                                                                                               Lindenbaum M, Greene A,
                                                                                                                                                                                                                                                                                                                                                                                             (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 43; Page 143; 272pp; English.
                                                                                                                                                                                                                                                                                                     10-MAY-2002; 2002WO-US17452
                                                                                                                                                                                                                                                                                                                                         30-MAY-2001; 2001US-294758P.
21-MAR-2002; 2002US-366891P
                                                                                                                                                                                                                                                                                                                                                                                                                             Perez C, Li
Shellard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-140461/13.
                                                                                                                                                                                                                                 WO200297059-A2.
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Stewart S,
                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              interest
                                                                                                                                                                                                                                                                                                                                                                                                                               Perkins
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The present invention describes a vector (I) comprising operably linked recipient cell, preferably in bacteria such as Ilowing replication in a recipient cell, preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising; (i) promoter or promoter region capable of being recognized by RNA polymerases of a ewkaryotic cell or by prokaryotic RNA polymerases; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyademylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or

New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.

Claim 12; Page 15; 104pp; English.

(CSIR ) COMMONWEALTH SCI & IND RES ORG.

Helliwell C;

Waterhouse P,

Wesley S,

WPI; 2002-682669/73.

cell, preferably a stem cell or an embryo. (II) comprises a heterologous mucleic acid that encodes a therapeutic product which is useful for making a library of Aces comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the

exemplification of the present invention.

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mammal) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinjection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for an aking a library of Aces comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                         Chromosome-based platform, artificial chromosome, eukaryotic chromosome, att site; integrase, recombinase, ACes, gene therapy; transgenic animal, platform artificial chromosome expression system; PCR primer, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleming
                                                                                                                                                                                     ;
                                                                                                                                                         Score 25; DB 25; Length 25;
Pred. No. 0.11;
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                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                Recombination site related oligonucleotide SEQ ID NO:56.
                                                                                                                                                                                     ..
                                                                                                                               Seguence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
                                                                                                                                                                                     0; Mismatches
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                                                                                                                                                                                                                 25
                                                                                                                                                                                                                                         1 Grrcagcrrrcrrgracaadrrdg 25
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                                                                                                                                                                                                                 1 GITCAGCITICITGIACAAGITGG
                                                                                                                                                           100.0%;
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2002US-366891P.
                                                                                                                                                                                                                                                                                                                ACC44665 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                     25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perez C, L. Shellard J;
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                                                                                                                                                                       Similarity
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21-MAR-2002;
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Stewart S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                            ACC44665;
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Best Local 9
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The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes. The invention of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, trNA, rDNA, structural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and proteins, and proteins, antipodies, no strokines, growth factors, antipodies, or stress in a plant. The resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that provides and agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant artificial chromosome; PAC; transgenic plant; vaccine;
blood factor; herbicide; stress; agronomical; nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
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0
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                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       Artificial plant chromosome related oligo SEQ ID No 42.
                                                                                                                                    100.0%; Score 25; DB 25; 100.0%; Pred. No. 0.11;
                                                                                                   Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
                                                                                                                                               100.0%; Prec. ...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perkins E;
                                                                                                                                                                                                                                1 GTTCAGCTTTCTTGTACAAAGTTGG
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                                                                                                                                                                                                                                                                                                                                   ABT16630 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                       25; Conservative
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                                                                                                                                        Query Match
Best Local Similarity
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ABT16630
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The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (1) a platform artificial chromosome expression system (ACes) (II) comprising several sites that participate in recombinase caralysed recombination; and (2) a method (M1) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (M1) is useful for introducing a heterologous nucleic acid molecule into a platform artificial artificial chromosome, preferably an ACes. (II) is useful for artificial chromosome, preferably an ACes. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammanl) by introducing (II) by cell fusion, lipical-mediated transfection by a carrier system, microbinection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic

Gaps

0;

Length 25; Indels

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The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transpanic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, tRNA, rDNA, structural proteins, marker proteins, lagands, receptors, ribozymes, therapeutic proteins, and in plant artificial proteins, vaccines, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistance to diseases, insects, herabloides, or stress in a plant. The reterologous nucleic acid optionally encodes a product that alters nutrient use and/or improves the nutrient engance and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (YAC). This polynucleotide sequence represents an oligo relating to the method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant artificial chromosome, PAC, transgenic plant; vaccine,
blood factor, herbicide, stress, agronomical, nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
chromosome (BAC) or a yeast artificial chromosome (YAC). This polynuclectide sequence represents an oligo relating to the method for producing plant artificial chromosomes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more regions with equivalent amounts of euchromatic and heterochromatic nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                  Artificial plant chromosome related oligo SEQ ID No 47.
                                                                                                                                                   0;
                                                                                                              100.0%; Score 25; DB 25; 100.0%; Pred. No. 0.11;
                                                                           Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHROMOS MOLECULAR SYSTEMS INC. AGRISOMA INC.
                                                                                                                                                                                          1 GTICAGCTITCTIGIACAAAGTIGG 25
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                                                                                                                    100.0%; F.
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                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                         ABT16635 standard; DNA;
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les 25; Conser
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AASO6174-AASO6322 represent Bacteriophage lambda att recombination site nucleic acid sequences, and PCR primers of the invention. The att sequences are recognised by the recombination protein lambda att sequences are recognised by the recombination protein lambda integrase (Int). The invention is a new method of producing a population of hybrid nucleic acids comprising mixing at least a first population of nucleic acids comprising one or more recombination sites with at least causing some or all of the nucleic acids to recombine with all or some of the target nucleic acids. The method is useful for producing a population of hybrid nucleic acids which may be the same or different. The nucleic acids may be used to express therapeutic proteins or peptides and they may also be used to each sovel fusion proteins by expressing different sequences linked to each other. The method allows simultaneous cloning of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Producing hybrid nucleic acids, useful for expressing novel therapeutic polypeptides, by mixing the same or different nucleic acids having one or more recombination sites in the presence of recombination proteins,
                                                                                                                                                                                                                                                                                                                                                          recombination; att site; PCR primer; lambda Int;
                                                                                            Gaps
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                                                                                            Indels
                                                               Length
producing plant artificial chromosomes of the invention.
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0
                                                             100.0%; Score 25; DB 25; 100.0%; Pred. No. 0.11;
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                                Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
                                                                                              Mismatches
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                                                                                                                           1 GTTCAGCTTTCTTGTACAAGTTGG 25
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09-MAR-2000; 2000US-0188020.
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                                                                                                                                                                                                                                       AAS06183 standard; DNA; 27
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                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                            Bacteriophage lambda;
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BRASCH M A.
TEMPLE G F.
HARTLEY J L.
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                                                                                 Similarity
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Length 27;

DB 22;

Score 25; DB 22 Pred. No. 0.11;

100.0%;

Query Match Best Local Similarity

Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda

40200052027-A1

08-SEP-2000

Recombination site nucleotide sequence attP2.

(first entry)

11-JAN-2001

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the first population to recombine with the first target nucleic acid molecules to form a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a thirth population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. Sequences AB258727-762 represent att recombination site sequences used in the method of the
 ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        molecule
 Gaps
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                                                                                                                                                                                                                                                                                  recombination; nucleic acid selection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Inserting a population of nucleic acids into a second target for selecting and isolating nucleic acid molecules by mixing population of nucleic acid with a second target nucleic acid
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Indels
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 0; Mismatches
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                                  GTTCAGCTTTCTTGTACAAAGTTGG
                                                                                                                                                                                                                                                    Att site nucleotide sequence attP2.
                                                                                                                                                                                                                                                                                   Nucleic acid insertion, recombir
nucleic acid isolation; att; ds.
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                                                                                                                                                    ABZ58736 standard; DNA; 27
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Matches 25; Conservative
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Isolated nucleic acid molecules encoding an attB1, attB2, attP2, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the

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Cheo

Temple GF,

Brasch MA,

fartley JL,

WPI; 2000-543948/49.

(LIFE-) LIFE TECHNOLOGIES INC.

99US-0122389. 99US-0126049. 99US-0136744.

02-MAR-1999; 28-MAY-1999; 3-MAR-1999;

02-MAR-2000; 2000WO-US05432.

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The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nuclectides sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination sites and as escond att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination site and a second nucleic acid molecule least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising at second recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site attoresses with the mutated att recombination are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, classing lusion tages from desired proteins, operably linking nucleic acid molecules of interest to require to specially linking mucleic acid molecules of interest cephanging copy number, changing replicons, cloning into phages and cloning (1), (II), (III), host cells and vectors can be used in the present invention.
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ó,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 233 BP; 94 A; 35 C; 32 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       recombinational cloning of polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GITCAGCITICITGIACAAGTIGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 drichderricirdrachadride 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AACS5524 standard; DNA; 4165 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     o
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; Fig 9; 459pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC55524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 19
AAC5524/c
ID AAC555:
XX
AC AAC555:
XX
TT AC AAC555:
AC AAC555:
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g
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Gaps

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1 GTTCAGCTTTCTTGTACAAGTTGG 25

25

g

AAC55383 standard; DNA; 233 BP.

AAC55383;

RESULT 18 AAC55383/C ID AAC55 XX AC AAC55

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Bacteriophage lambda
                                            WPI; 2000-543948/49.
                  WO200052027-A1.
                               23-MAR-1999;
28-MAY-1999;
                             02-MAR-1999;
                      08-SEP-2000
              Synthetic
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The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 concoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 conclided molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination sites and a second att recombination site, and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination site some region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site in that interacts with the mutated comprising a second recombination site ond a second nucleic acid molecule comprising a second recombination site ond a second nucleic acid molecules of intracellular locations, leaving fusion targe fine nucleic acid molecules. They can be used for changing vectors, targeting send proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicans, claning into phages and claning (I), (III), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds. 100.0%; Score 25; DB 21; Length 4204; 100.0%; Pred. No. 0.18; Sequence 4204 BP; 1198 A; 912 C; 959 G; 1135 T; 0 other; 0; Mismatches Donor plasmid pDONR202 nucleotide sequence Brasch MA, Temple GF, Example 9; Fig 50; 459pp; English (LIFE-) LIFE TECHNOLOGIES INC. 32-MAR-2000; 2000WO-US05432. 99US-0122389. 99US-0126049. 25; Conservative Bacteriophage lambda WPI; 2000-543948/49. Best Local Similarity WO200052027-A1 23-MAR-1999; 28-MAY-1999; 32-MAR-1999; Hartley JL, 08-SEP-2000 Synthetic Query Match Matches ਨੇ ö mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (1), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, and attB2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising or merca at recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second attractombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated attracombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the Bacteriophage lambda; att; recombination site; attB; attR; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds. attP2, regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. Gaps Isolated nucleic acid molecules encoding an attB1, attB2, attP1, a attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -. 0 100.0%; Score 25; DB 21; Length 4165; 100.0%; Pred. No. 0.18; 0; Indels 0 Sequence 4165 BP; 1117 A; 926 C; 925 G; 1196 T; 1 other; Cheo D; Donor plasmid pDONR204 nucleotide sequence. 2209 GITCAGCTTTCTTGTACAAAGTTGG 2185 1 GITCAGCTITCTTGTACAAGTIGG 25 Temple GF, Example 9; Fig 52; 459pp; English (LIFE-) LIFE TECHNOLOGIES INC 99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-2000; 2000WO-US05432 Query Match
Best Local Similarity 100.
Matches 25; Conservative Hartley JL, Brasch MA,

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Cheo

; 0 Gaps ö 0; Indels 2248 GTTCAGCTTTCTTGTACAAAGTTGG 2224 1 GITCAGCITICITGIACAAGTIGG 25 AAC55523 standard; DNA; 4208 BP 11-JAN-2001 (first entry) AAC55523; RESULT 21 AAC55523 X X X X

AAC55522 standard; DNA; 4204 BP.

RESULT 20 AACS5522/c

11-JAN-2001 (first entry)

AAC55522;

HXXXX

. 0.18;

Nucleic acid insertion; recombination; nucleic acid selection; nucleic acid isolation; ds.

40200295055-A2

Synthetic.

28-NOV-2002

Destination plasmid pDONR212 nucleotide sequence

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the present invertible interpretation artification and attract action and attract action and attract nucleotide sequence. Also described are: (1) an isolated nucleic acid nucleotide sequence. Also described are: (1) an isolated nucleic acid nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (11) comprising one or more act recombination site and a second attraction between the recombination site and a second attraction between the recombination site acid molecule (III) comprising one or more mutated attracombination site acid molecule comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising a second recombination site and a second nucleic acid molecule attracembination site. (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of attraceombinations. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to required to proteins, constructing genes for tusion proteins, changing recombinations and methods are required proteins, operably linking nucleic acid molecules of interest to required the present invention are used for this proteins, operably linking nucleic acid molecules of interest to require the present interactions of agence for this proteins, changing recombinations and methods of interest to a regulatory genetic sequences, constructing genes for tusion proteins, changing recombinations and methods of interest to a required the present interactions of an interest constructing genes for tusion proteins, changing recombinations and methods and m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
                                                                      Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes isolated nucleic acid molecules (I)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 4208 BP; 1172 A; 997 C; 875 G; 1164 T; 0 other;
                     Donor plasmid pDONR203 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 9; Fig 51; 459pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (LIFE-) LIFE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2000; 2000WO-US05432.
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les 25; Conservative
                                                                                                                                                                                                         Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-543948/49
                                                                                                                                                                                                                                                                                              MO200052027-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-MAR-1999;
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28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                              Synthetic
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Matches
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Cheo

Temple GF,

Brasch MA,

99US-0122389. 99US-0126049. 99US-0136744.

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The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid with a second population, (c) mixing the second population of nucleic acid, and (d) causing some or all of the nucleic acid, and (d) causing some or all of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR212 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                            Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 25; Length 4428;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4428 BP; 1214 A; 1064 C; 929 G; 1221 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
                                                                                                                                                                                                                                                                      Byrd DRN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Donor plasmid pDONR201 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                      Esposito D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3180 GITCAGCITICITIGIACAAAGITGG 3204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 27B-C; 273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GITCAGCITICITGIACAAAGIIGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC55521 standard; DNA; 4470 BP
                                                                                                                                                                            21-MAY-2002; 2002WO-US15947.
                                                                                                                                                                                                           21-MAY-2001; 2001US-291973P
                                                                                                                                                                                                                                                                      Li X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Conservative
                                                                                                                                                                                                                                         (INVI-) INVITROGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriophage lambda.
                                                                                                                                                                                                                                                                                                      WPI; 2003-129436/12.
                                                                                                                                                                                                                                                                         Cheo D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200052027-A1
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                                                                                                                                                                                                                                                                         Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC55521;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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AAC55521
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Gaps

0;

100.0%; Score 25; DB 21; Length 4208; 100.0%; Pred. No. 0.18; or Indels 0; Mismatches 0; Indels 0;

Db

ABZ58768 standard; DNA; 4428 BP.

(first entry)

01-MAY-2003

ABZ58768;

RESULT 22 ABZ58768 ID ABZ58 XX AC ABZ58 XX DT 01-MA

.. 0

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Destination plasmid pDONR201 nucleotide sequence.
                                                                                                                                                                                                                                                                                                  Query Match
100.0%; Score 25;
Best Local Similarity 100.0%; Pred. No. 6
Matches 25; Conservative 0; Mismatch
                                                                                                                                                                                                                                                                                                                                            2343 GITCAGCITICITGIACAAGIIGG 2367
                                                                                                                                                                                                                                                                                                                              1 GTTCAGCTTTCTTGTACAAAGTTGG 25
                                                                                                           Example 9; Fig 49; 459pp; English
                                       (LIFE-) LIFE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                             ABZ58767 standard; DNA; 4470
            99US-0122389.
99US-0126049.
99US-0136744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-MAY-2002; 2002WO-US15947.
02-MAR-2000; 2000WO-US05432.
                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                     Brasch MA,
                                                                  WPI; 2000-543948/49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO200295055-A2
                                                                                                                                                                                                                                                                                                                                                                                                        01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-NOV-2002.
                   23-MAR-1999;
28-MAY-1999;
             32-MAR-1999;
                                                      Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                           ABZ58767;
                                                                                                                                                                                                                                                                                                                                                                 RESULT 24
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The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid with a second population; (c) mixing the second population or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR201 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid -
                                                                                                                                                                                           Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid insertion; recombination; nucleic acid selection; nucleic acid isolation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 25; Length 4470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Destination plasmid pDONR212(F) nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Esposito D, Byrd DRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 0.18;
                                                                                                    Byrd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25;
                                                                                                    Esposito D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2343 GTTCAGCTTTCTTGTACAAGTTGG 2367
                                                                                                                                                                                                                                                                                                    Disclosure; Fig 26B-C; 273pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GITCAGCITICTIGIACAAGTIGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABZ58769 standard; DNA; 4627 BP
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21-MAY-2001; 2001US-291973P.
                                                                                                    Li X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.
Best Local Similarity 100.
Matches 25; Conservative
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                                                  (INVI-) INVITROGEN CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-129436/12
                                                                                                    Cheo D,
                                                                                                                                                   WPI; 2003-129436/12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                    Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABZ58769;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABZ58769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conciding an attB1, attB2, attB1, attB2, attB1, and attB2 nucleotide sequence. Also described are: (1) an isolated nucleic acid nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (11) comprising one or more att recombination sites comprising to finteraction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule (III) comprising as second recombination site and a second nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising the mutated attrecombination site that interacts with the mutated comprising a second recombination site that interacts with the mutated attrecombination site that interacts with the mutated comprising a second recombination site that interacts with the mutated attrecombination site that interacts with the mutated comprising a second recombination site that interacts with the mutated attrecombination site in the recombinational cloning of nucleic acid molecules. They can be used for changing vegetors, targeting genes products to intracellular locations, cleaving fusion tages from cegning copy number, changing replicons, cloning into phages and cloning. (I) (II), (II), host cells and vectors can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                          attP2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             present invention describes isolated nucleic acid molecules (I)
                                                                                                                                                                                                                                                                                                       Isolated nucleic acid molecules encoding an attB1, attB2, attP1, a
attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
recombinational cloning of polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acid insertion; recombination; nucleic acid selection; nucleic acid isolation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21; Length 4470;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.18;
                                                                                                                                                                                                        Cheo D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                             Temple GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВР
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Disclosure; Fig 28B-C; 273pp; English.

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Gaps

; 0

The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid with a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid  ${ t pDONR212}(F)$  nucleotide sequence Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 other; 8888888888888888888

DB 25; Length 4627; 0.18; 0; Indels 0; Mismatches Score 25; Pred. No. ( 100.0%; 25; Conservative Query Match Best Local Similarity Matches

2331 Grickácrirchrátacaaácrica 2355 1 GTTCAGCTTTCTTGTACAAGTTGG 25 ò

AB258770; RESULT 26 ABZ58770 

ABZ58770 standard; DNA; 4627

(first entry) 01-MAY-2003 Destination plasmid pDONR212(R) nucleotide sequence.

Nucleic acid insertion; recombination; nucleic acid selection; nucleic acid isolation; ds.

Synthetic.

WO200295055-A2.

28-NOV-2002

21-MAY-2002; 2002WO-US15947.

21-MAY-2001; 2001US-291973P.

(INVI-) INVITROGEN CORP.

WPI; 2003-129436/12.

Cheo D, Li X,

Brasch MA,

Esposito D, Byrd DRN;

Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the secor population of nucleic acid with a second target nucleic acid -

Disclosure; Fig 29B-C; 273pp; English

The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid with a second population, (c) mixing the second population of nucleic acid with a second target nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR212(R) nucleotide sequence.

Sequence 4627 BP; 1262 A; 1126 C; 990 G; 1249 T; 0 other;

ö Gaps ; 0 Length 4627; 0; Indels 100.0%; Score 25; DB 25; 100.0%; Pred. No. 0.18; ive 0; Mismatches 0; 2331 GTTCAGCTTTCTTGTACAAAGTTGG 2355 25 Query Match Best Local Similarity 100. Matches 25; Conservative dd à

RESULT 27 AAC55525

AAC55525 standard; DNA; 4939

11-JAN-2001 (first entry)

ö

Gaps

. 0

AAC55525;

Donor plasmid pDONR205 nucleotide sequence.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda

Synthetic

WO200052027-A1.

08-SEP-2000

02-MAR-2000; 2000WO-US05432.

02-MAR-1999;

99US-0122389. 99US-0126049. 99US-0136744. 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC.

Temple GF, Brasch MA, Hartley JL,

á

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attB2, attL1, attL2, attR1, and attR2 nuclectide sequence useful for the recombinational cloning of polypeptides -

Example 10; Fig 53; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, an isolated nucleic acid molecule (II) comprising one or more mutated att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination site and a second nucleic acid molecule (III) comprising a second recombination site and a second nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecules. They can be used for the recombination site (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of seconds recombination site and second for changing vectors, targeting desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing replicons, cleaning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the conding. (I), (III), host cells and vectors can be used in the used in the exemplification of the present invention. 

Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 other;

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0
                             Gaps
                             ·,
 DB 21; Length 4939;
100.0%; Score 25; DB 21; Length 4
100.0%; Pred. No. 0.18;
iive 0; Mismatches 0; Indels
                                 Conservative
                 Similarity
   Query Match
Best Local Simi
Matches 25;
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938 GTTCAGCTTTCTTGTACAAAGTTGG 962 25 1 GITCAGCTITCTTGTACAAGTIGG g

AAC55526 standard; DNA; 5156

AAC55526;

(first entry) 11-JAN-2001 Donor plasmid pDONR206 nucleotide sequence.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda Synthetic

WO200052027-A1.

08-SEP-2000.

02-MAR-2000; 2000WO-US05432

99US-0122389. 99US-0126049. 99US-0136744. 23-MAR-1999; 28-MAY-1999; 02-MAR-1999;

(LIFE-) LIFE TECHNOLOGIES INC.

Cheo

Temple GF, Hartley JL, Brasch MA,

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 9; Fig 54; 459pp; English.

nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning, (1), (11), (11), (nst cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. The present invention describes isolated nucleic acid molecules (I) encoding an attBl, attB2, attBl, attB2, attLl, attL2, attB1, and attR2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (II) comprising one or more mutated att recombination sites and (III) comprising one or more mutated att recombination sites one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination describe and a second nucleic acid molecule. comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of 

Sequence 5156 BP; 1413 A; 1183 C; 1216 G; 1342 T; 2 other;

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ö
                                Gaps
                               0;
Length 5156;
                                0; Indels
 DB 21;
Query Match
100.0%; Score 25; DB 21
Best Local Similarity 100.0%; Pred. No. 0.18;
Matches 25; Conservative 0; Mismatches
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Gricagcrircrigiacaaagrieg 3176

8

RESULT 29 AAC55632/

AAC55632 standard; DNA; 5584

BP.

AAC55632;

(first entry) 11-JAN-2001

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds. Donor plasmid pDONR207 nucleotide sequence.

Bacteriophage lambda Synthetic.

WO200052027-A1.

02-MAR-2000; 2000WO-US05432. 08-SEP-2000 

99US-0122389. 02-MAR-1999;

99US-0126049. 23-MAR-1999;

28-MAY-1999;

(LIFE-) LIFE TECHNOLOGIES INC.

Cheo D; Temple GF, Brasch MA, Hartley JL,

WPI; 2000-543948/49.

attP2, Isolated nucleic acid molecules encoding an attB1, attB2, attP1,  $^{\epsilon}$  attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Disclosure; Fig 97; 459pp; English

included an attB1, attB2, attP1, attB2, attL1, attL1, attL1, attB2, attB2, attP1, attB2, attL1, attL1, attL1, attB2, attB2, attP2, attL1, attL1, attL1, attB2, attB2, attP2, attL1, attL1, attL1, attB2, attB2, attP2, attL1, attL1, attL2, attL1, attB2, attB2, attP2, attL1, attL1, attL2, attL1, attB2, attB changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. present invention describes isolated nucleic acid molecules (I)

Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 other;

Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds.

Acceptor vector pHELLSGATE nucleotide sequence SEQ ID NO:13.

11-DEC-2002 (first entry)

ABQ82130;

us-10-055-001a-11.rng

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The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid with a second population; (c) mixing the second population of nucleic acid with a second population to recombine with second target nucleic acid; and (d) causing some or all of the nucleic acid molecules of the second population to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence
                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid -
                                   Gaps
                                 .
0
                                                                                                                                                                                                                                                                                                                                   Nucleic acid insertion; recombination; nucleic acid selection; nucleic acid isolation; ds.
 DB 21; Length 5584;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   represents the donor plasmid pDONR207 nucleotide sequence.
                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Byrd DRN;
                                   ;
0
              0.18;
                                                                                                                                                                                                                                                                                                     Donor plasmid pDONR207 nucleotide sequence.
Query Match
100.0%; Score 25; DE
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Esposito D,
                                                                                            3243 GTTCAGCTTTCTTGTACAAAGTTGG 3219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 18B-C; 273pp; English
                                                                    25
                                                                    1 GITCAGCTITCTIGIACAAAGTIGG
                                                                                                                                                                                               ABZ58766 standard; DNA; 5584 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-MAY-2002; 2002WO-US15947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-MAY-2001; 2001US-291973P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cheo D, Li X,
                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (INVI-) INVITROGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-129436/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 25; Consera
                                                                                                                                                                                                                                                                                                                                                                                                                              WO200295055-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                  ABZ58766;
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New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.

(CSIR ) COMMONWEALTH SCI & IND RES ORG.

26-JAN-2001; 2001US-264067P. 29-NOV-2001; 2001US-333743P. 24-JAN-2002; 2002WO-AU00073

WO200259294-A1. 01-AUG-2002.

Synthetic

Waterhouse P, Helliwell C;

Wesley S,

WPI; 2002-682669/73.

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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a cukaryotic cell or by prokaryotic RNA polymerases of a third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and polyadenylation region functional in the eukaryotic cell. The first and polyadenylation region functional in the eukaryotic cell. The first cand preferably are identical. The first and second and third recombination free the third and fourth recombination site, and second recombination site, and preferably are identical. The first and second recombination site, or the third and fourth recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used conventional breeding scheme to produce more plants with the same conventional breeding scheme to produce more plants with the same recombined with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same recombined which a minerial side of the convention of the conv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 24; Length 18691;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 100.0%; Score 25; DB 2. Similarity 100.0%; Pred. No. 0.2; 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14520 GTTCAGCTTTCTTGTACAAAGTTGG 14544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTTCAGCTTTCTTGTACAAGTTGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 13; Page 62-72; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABQ82130 standard; DNA; 18691 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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Gaps

.; 0

100.0%; Score 25; DB 25; Length 5584; 100.0%; Pred. No. 0.18; Ative 0; Mismatches 0; Indels 0.

3243 GTTCAGCTTTCTTGTACAAAGTTGG 3219

Dp

ABQ82130 standard; DNA; 18691 BP.

RESULT 31 ABQ82130 ID ABQ8 XX

1 GTTCAGCTTTCTTGTACAAGTTGG

Conservative

25

Oligonucleotide #43 for recombination and cloning method Cloning; donor; recombination site; vector; chimeric;

Temple GF;

Hartley JL,

Brasch MA, Fox DK, WPI; 1999-303011/25

(LIFE-) LIFE TECHNOLOGIES INC

98US-0177387. 97US-0065930.

98WO-US22589.

36-OCT-1998; 23-OCT-1998; 24-OCT-1997;

W09921977-A1

Synthetic.

06-MAY-1999

Disclosure, Page 171; 185pp; English.

New nucleic acid cloning methods

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New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target transletic acids and for producing large amounts of double-stranded RNA -
                                    Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 24; Length 18691; 100.0%; Pred. No. 0.2;
                  Acceptor vector pHELLSGATE nucleotide sequence SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16418 GITCAGCITICITGIACAAGTIGG 16394
                                                                                                                                                                             (CSIR ) COMMONWEALTH SCI & IND RES ORG.
                                                                                                                                                                                                Helliwell C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTTGTACAAAGTTGG 25
                                                                                                                             24-JAN-2002; 2002WO-AU00073.
                                                                                                                                                26-JAN-2001; 2001US-264067P.
29-NOV-2001; 2001US-333743P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX78977 standard; DNA; 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25; Conservative
                                                                                                                                                                                                                    WPI; 2002-682669/73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                       WO200259294-A1.
                                                                                                          01-AUG-2002
                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX78977;
                                                                                                                                                                                                  Wesley S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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ID AAX7

XX

AC AAX7

XX

DT 17-A
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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell; preferably in bacteria such as Escherichia col; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a cukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and polyadenylation sites, (iii) 3' transcription termination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each the third and fourth recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants

convert a DNA fragment into an inverted repeat structure. Plants

conventional breeding scheme to produce more plants with the same conventional breeding scheme to prime mine produce a chimeric general resource.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention.
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Claim 13; Page 62-72; 104pp; English.
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The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NAMS) comprising: (a) combining in vitro or in vivo: (l) at least one insert donor molecules (IDMS) comprising one or more desired nucleic acid segments flanked by at least 2 comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMS) comprising at least 2 recombination converse which do not recombine with each other; and (3) one or more sites which do not recombine with each other; and (3) one or more sites which do not recombine with each other; and (3) one or more sites which do not recombine with each other; and (3) one or more when or more of the desired segments into one or more of the methods can be used for the efficient and specific recombination of NAM segments. They can be used for changing vectors. The onethods can also be used for changing vectors. The oligonucleotides have the desired used for changing vectors. The oligonucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               att recombination site; core region; mutation; enhance; recombination; vector; subcloning; regulation; exchange; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.2%; Score 23.8; DB 20; Length 25; 88.0%; Pred. No. 0.37; ive 3; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25 BP; 4 A; 3 C; 5 G; 10 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GIICAGCIIICIIGIACAAAGIIGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      attPl core region.
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Best Local
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AAT48210-25 are att recombination site core region DNA sequences. The core region has at least one engineered mutation that enhances recombination in vitro in the formation of a Cointegrate or Product DNA. These core regions can be incorporated into novel vector donor DNA molecules. The nucleic acids, vectors and methods of the invention are used to obtain chimeric nucleic acid using recombination proteins and engineered recombination sites in vitro or in vivo. The improved specificity, speed and yields of the invention facilitates DNA or RNA subcloning, regulation or exchange useful for any related purpose; e.g. in vitro recombination of DNA segments, and in vitro or in vivo insertion or modification of transcribed, replicated, isolated or genomic DNA or
                                                                                                         Nucleic acids, vectors and methods to obtain chimeric nucleic acid
using recombinant proteins and engineered recombination sites in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oligonucleotide #15 for recombination and cloning method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cloning; donor; recombination site; vector; chimeric; ss.
                                                                                                                                                                                                                                                                                                                                                                                                          Score 23.4; DB 18;
Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                 Seguence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Temple GF
                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GTTCAGCTTTCTTGTACAAGTTGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Gricagcrirrirgiacaaagrieg 25
                                                                                                                                                                  Claim 14; Page 56; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fox DK, Hartley JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                          (LIFE-) LIFE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0177387.
97US-0065930.
                                                                                                                                                                                                                                                                                                                                                                                                             93.6%;
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95US-0486139.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Conservative
                                                     Brasch MA, Hartley JL;
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                                                                                WPI; 1997-065168/06
                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                          or in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LIFE-) LIFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-OCT-1998;
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07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAX78949;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 35
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The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NAMS) comprising: (a) combining in vitro or

Disclosure; Page 162; 185pp; English.

New nucleic acid cloning methods

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Gaps

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Indels

Length 25;

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0;
in vivo: (1) at least one insert donor molecules (IDMs) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMs) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or more site-specific recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the wethods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method for apposing an expression signal and a gene or partial gene, using recombinatorial cloning. The method incubates nucleic acids comprising the expression signal and the gene/ partial gene in the presence of a recombination protein under conditions sufficient to cause recombination and therefore appose the expression signal and the gene or partial gene. The methods are useful for apposing an expression signal and a gene or partial gene using recombinatorial cloning. The methods are also useful for changing vectors, constructing enes for fusion proteins, changing copy number, changing replicons, cloning into phages, and cloning e.g., PCR products (with an attB site at one end and a loxP site at the other end), genomic DNAs, and cDNAs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Methods for apposing nucleic acids comprising an expression signal ar
a gene/partial gene, using recombinatorial cloning by incubating the
nucleic acids in the presence of a recombination protein under
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombination site; copy number; replicon; recombinatorial cloning;
                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                   Length 25;
                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                   Score 23.4; DB 20;
Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                              Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                              25
                                                                                                                                                                                                                                                                                                                                                                                                                 Gricageriririgiacaaagrieg 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 14; Column 18; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                              1 GITCAGCITICTIGIACAAAGTIGG
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombination site attP1 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conditions for recombination
                                                                                                                                                                                                                                                                                                     93.6%;
ilarity 96.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96US-0663002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAD14443 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INVI-) INVITROGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brasch MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488248/53.
                                                                                                                                                                                                                                                                                                                        Local Similarity
nes 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US6270969-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD14443;
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD14443
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The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors acch comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture; and selecting for a host comprising the chimeric nucleic acid molecule, and selecting gainst a host comprising the vectors comprising the second vector; to clone the nucleic acid. The present sequence is a recombinantion site, which may be used in the method of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host
The methods are highly specific, rapid, and less labour intensive than prior art methods. The present sequence is a recombination site useful for recombination cloning.
                                                                                                                               Gaps
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0
                                                                                             Length 25;
                                                                                                                             Indels
                                                                                             Score 23.4; DB 22;
Pred. No. 0.56;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
                                                               Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
                                                                                                                             0; Mismatches
                                                                                                                                                           25
                                                                                                                                                                                           GITCAGCITITITIGIACAAAGITGG 25
                                                                                                                                                                                                                                                                                                                                                                                                     Recombination site; cloning; att; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 25; Column 46; 73pp; English.
                                                                                                                                                              GTTCAGCTTTCTTGTACAAAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LIFE-) LIFE TECHNOLOGIES INC
                                                                                               93.6%;
96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96US-0663002.
95US-0486139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0005476.
                                                                                                                                                                                                                                                                        AAF55749 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                     Recombination site attPl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brasch MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-136877/14.
                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Unidentified
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                                                                                                                             24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hartley JL,
                                                                                           Query Match
Best Local S
                                                                                                                                                                                                                                                                                                         AAF55749;
                                                                                                                               Matches
                                                                                                                                                                                                                                           RESULT 37
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The present invention describes an isolated mucleic acid molecule (I) comprising a first nucleic acid sequence having a defined sequence (AACB7866 to AACB7881, sequences complementary to AACB7881. Or an RNA sequence corresponding to AACB7866 to AACB7881. Also described are: (I) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site or avoids hairpin formation, the recombination site of a recombination site of a site (I) an isolated nucleic acid molecule (III) comprising a first att recombination site comprising a mutation that comprising a first att recombination site comprising a mutation that above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids; and (4) cells comprising the above mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining engineered recombination in vitro or in vivo makes the methods for NNA or RNA subcloning, highly specific, rapid, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank a selectable marker and comprise a core region having an engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                 Escherichia coli core region recombinant site attP1 SEQ ID NO:15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                      Core region, recombination site, cloning, chimeric DNA, characteristic, mutation, att site, lox site, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <u>..</u>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23.4; DB Pred. No. 0.56; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GITCAGCTTTCTTGTACAAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    claim 1; Column 18; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ82127 standard; DNA; 25 BP.
                             AAC87880 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                      (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                96US-0663002.
98US-0005476.
95US-0486139.
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96.0%;
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                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brasch MA, Hartley JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        less labour intensive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NPI; 2001-049004/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                           Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                  07-JUN-1996;
12-JAN-1998;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                  20-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                   02-MAR-2001
                                                                                                                                                                                                                                                            US6143557-A
                                                                                                                                                                                                                                                                                                 07-NOV-2000
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                                                                  AAC87880;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mutation
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ID ABQ6
XX
AC ABQ6
RESULT 38
                  4AC87880
                                 %%CGGGGGGGGGGGCX%%HHHHHXXHXHXBXHXBXGXGXXXXXXXBHXXBXXBX
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ABQ82127

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Gaps

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Indels

1;

0; Mismatches

24; Conservative

Matches

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Local Similarity

Query Match

1 GTTCAGCTTTCTTGTACAAGTTGG 25 GITCAGCITITITIGIACAAAGIIGG 25

93.6%; Score 23.4; DB 22; Length 25; 96.0%; Pred. No. 0.56;

Chromosome, based platform, artificial chromosome; eukaryotic chromosome, att site; integrass, recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; PCR primer; ss.

Synthetic

construct; recombinational cloning; silencing;

Recombination site related oligonucleotide SEQ ID NO:55.

29-MAY-2003 (first entry)

ы.

Fleming

(first entry)

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Core sequence of recombination site attP1 SEQ ID NO:10.
                     Chimeric nucleic acid construct; recombinational cl recombination site; double stranded RNA; plant; ss.
                                                                       26-JAN-2001; 2001US-264067P.
29-NOV-2001; 2001US-333743P.
                                                              24-JAN-2002; 2002WO-AU00073
                                                                                                       WPI; 2002-682669/73
                                             WO200259294-A1
                                                      01-AUG-2002
                                    Synthetic
                                                                                              Wesley S,
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The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (I) a platform artificial chromosome cappression system (ACes) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (MI) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for introducing a heterologous nucleic acid molecule into a platform artificial chromosome, preferably an ACes. (II) is useful for producing catificial chromosome, preferably an ACes. (II) is useful for producing carrier system, microinjection, microcall fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic microprojectile bombardment or direct DNA transfer into an embryonic coll, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612 con ACC44732 and ABP96650 to ABP96657 represent sequences used in the construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lindenbaum M, Greene A, Leung J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23.4; DB 25;
Pred. No. 0.56;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHRO-) CHROMOS MOLECULAR SYSTEMS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 43; Page 143; 272pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93.68;
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Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  30-MAY-2002; 2002WO-US17452.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2001; 2001US-294758P.
21-MAR-2002; 2002US-366891P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perez C, Li
Shellard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-140461/13.
                                                                                                                                                                                                                                                                                   WO200297059-A2
                                                                                                                                                                                                                                                                                                                                            05-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Perkins E,
Stewart S,
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à
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present introduction describes a vector (1) complitatory introduction in a recipient cell, preferably in bacteria such as Escherichia coli; (1) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter or cell; and (c) a chimeric DNA construct comprising: (i) promoter or cell; and color prokaryotic RNA polymerases of a chimeric DNA prokaryotic RNA polymerases of a chiral dand fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and polyadenylation region functional in the eukaryotic cell. The first can fourth recombination sites; (iii) 3' transcription termination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombination site, or producing large amounts of double-stranded RNA which can be used for producing large amounts of double-stranded RNA which can be used for producing large uncluded sequences. The vector is useful for convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used to conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric general sequence represents the convention of the phenotypic expression of nucleic acids. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CSIR ) COMMONWEALTH SCI & IND RES ORG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterhouse P, Helliwell C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 12; Page 15; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Conservative
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Gaps

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ACC44664 standard; DNA; 25 BP.

RESULT 40 ACC44664

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ACC44664;

SAXBX

Query Match Best Local Similarity

Matches

Length 25; Indels

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November 6, 2003, 23:06:49; Search time 102.25 Seconds (without alignments) 780.185 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Published Applications NA:*

1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW PUB.seq:*
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5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
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13: /cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US09_NEW PUB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
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17: /cgn2_6/ptodata/1/pubpna/US10A_NEW_PUB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2141354 seqs, 1595478879 residues
                                                                                                                                                                                                                                                                                                                                                                                                                    1 gttcagctttcttgtacaaagttgg 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                 US-10-055-001A-11
25
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Maximum DB seq length: 2000000000
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
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                                                                                                                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES	Description	Sequence 16, Appl	Sequence 8, Appli	Sequence 16, Appl	Sequence 16, Appl	Sequence 11, Appl	Sequence 16, Appl	Sequence 16, Appl	Seguence 16, Appl	Sequence 6, Appli	Sequence 11, Appl	Sequence 11, Appl	Sequence 16, Appl	Sequence 11, Appl	Sequence 16, Appl	Sequence 51, Appl	Sequence 56, Appl
	QI	US-09-855-797A-16	US-09-822-634-8	US-09-907-900-16	US-09-907-719-16	US-09-432-085-11	US-09-432-085-16	US-09-985-448-16	US-10-300-892-16	US-10-055-001A-6	US-10-055-001A-11	US-10-058-292-11	US-10-058-292-16	US-10-162-879-11	US-10-162-879-16	US-10-161-403-51	US-10-161-403-56
	DB	6	10	10	10	11	11	12	12	14	14	14	14	14	14	14	14
	* Query Match Length DB	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25
	% Query Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25
	Result No.	 	7	e	4	ഗ	9	7	60	σ	10	11	12	13	14	15	16

Sequence 10, Appl	Sequence 34, Appl	62	Seguence 21, Appl	63	Sequence 64, Appl		23	23	13	Sequence 13, Appl	Sequence 43, Appl	Sequence 43, Appl	Sequence 43, Appl	Sequence 43, Appl		Sequence 15, Appl		12	15	Sequence 15, Appl	15	Sequence 10, Appl	15	ä	Sequence 55, Appl	Sequence 6, Appli	Sequence 30, Appl	Sequence 21, Appl
US-09-732-914-10	US-10-151-690-34	US-10-151-690-62	US-10-151-690-21	US-10-151-690-63	US-10-151-690-64	US-10-151-690-61	US-10-055-001A-23	US-10-055-001A-23	US-10-055-001A-13	US-10-055-001A-13	US-09-855-797A-43	US-09-907-900-43	US-09-907-719-43	US-09-985-448-43	US-10-300-892-43	US-09-855-797A-15	US-09-907-900-15	US-09-907-719-15	US-09-432-085-15	US-09-985-448-15	US-10-300-892-15	US-10-055-001A-10	US-10-058-292-15	US-10-162-879-15	US-10-161-403-55	US-09-732-914-6	US-10-151-690-30	US-10-151-690-21
σ	14	14	14	14	14	14	14	14	14	14	σ	10	10	12	12	σ	10	10	11	12	12	14	14	14	14	6	14	14
27	27	4428	4470	4627	4627	5584	17862	17862	18691	18691	25	25	25	25	25	25	25	25	25	25	25	25	25	25	25	27	27	4470
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	95.2	95.2	95.2	95.2	95.2	93.6	93.6	93.6	93.6	93.6	93.6	93.6	93.6	93.6	93.6	93.6	93.6	93.6
25	25	52	25	25	25	25	25	25	25	25	23.8	23.8	23.8	23.8	23.8	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4	23.4
17	18	116	20	21	22	c 53	24	c 25	26	C 27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	c 45

## ALIGNMENTS

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RESULT 1
US-00-855-797A-16

Sequence 16, Application US/09855797A

Sequence 16, Application US/09855797A

Sequence 16, Application US/09855797A

Sequence 16, Application US/09855797A

Setematical INFORMATION:
APPLICANT: Hartley, Michael A.

APPLICANT: Hartley, Michael A.

APPLICANT: Parach, Michael A.

APPLICANT: Parach, Michael A.

APPLICANT: Prox, Donna K.

TITLE OF INVENTION: Recombination Sites

CURRENT APPLICATION NUMBER: US/09/855,797A

CURRENT APPLICATION NUMBER: US/00-05-16

PRIOR PRILNG DATE: 1999-04-22

PRIOR PRILNG DATE: 1999-04-22

PRIOR PLING DATE: 1999-04-22

PRIOR PLING DATE: 1999-10-24

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 16

LANGHIA: STATUME

TEARTH: 25

TYPE: DNA

OCHER INFORMATION: Description of Unknown Organism: recombination

OTHER INFORMATION: Products

US-09-085-197A-16

DOETY MATCH

BEST LOCAL Similarity 100.0%; Score 25; DB 9; Length 25;

Best Local Similarity 100.0%; Pred. No. 0.05;

Matches 25; Conservative 0, Mismatches 0; Indels 0; Gaps 0
```

RESULT 2

8 8

; 0

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APPLICANT: Hartley, James L.
APPLICANT: Bratley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
FILE REPREMENCE: 0942.2850004
CURRENT PELING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN VET: 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VS-09-432-085-11
Sequence 11, Application US/09432085
Publication No. US20030100110A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered;
TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington.
STATE: DC.
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATENIL RPC COMPA:
SOFTWARE: Patentin Release #1.0, Version #1.30
SUSTEMNT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
TT.NG DATE: (Herewith)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 25; DB 10;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GIICAGCITICITGIACAAAGIIGG 25
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APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
Publication No. US20020192819Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 09/00
FILING DATE: 12-JAN-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-907-719-16
                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 16
LENGTH: 25
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GENERAL INFORMATION:
APPLICANT: Hartley.
APPLICANT: Hartley.
APPLICANT: Temple, Gary F.
APPLICANT: Town M.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT FILING DATE: 2001-07-19
FRIOR PPLICATION NUMBER: 09/177,387
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PALENTIN VOI. 2.0
SEQ ID NO 16
ILENGTH: 25
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US-09-907-900-16
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100.0%; Score 25; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels
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                                                  GENERAL INCRMATION:
APPLICANT: Vile, Richard G.
APPLICANT: Harrington, Kevin
APPLICANT: Bareman, Andrew
APPLICANT: Bareman, Andrew
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
FILE REFERENCE: 07039-289001
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 06/193,977
PRIOR PELICATION NUMBER: 60/193,977
PRIOR PELICATION NUMBER: 60/193,977
PRIOR PELICATION NUMBER: 60/193,977
SPIOR PELICATION NUMBER: 60/193,977
SPIOR PELICATION NUMBER: 06/193,977
FILE FESTERE FASTER OF MINGOWS VERSION 4.0
SEQ ID NO 8
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: Synthetically generated vector sequence US-09-822-634-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GIICAGCITICITGIACAAGTIGG 25
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US-09-907-719-16
; Sequence 16, Application US/09907719
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Patent No. US20020172997A1
                          Sequence 8, Application US/09822634
Patent No. US20020150556A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
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Best Local Similarity
Matches 25; Conserv
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1 GTTCAGCTTTCTTGTACAAAGTTGG 25
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Publication No. US20030175970A1
GENERAL INFORMATION:
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-432-085-16
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Best Local
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Publication No. US20030100110A1

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
ITILE OF INVENTION: Recombinational Cloning Using Engineered
ITILE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 11; Length 25; 100.0%; Pred. No. 0.05;
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
FILING DATE: (Berewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1999
CLASSIFICATION:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1996
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION
PRIOR APPLICATION
CLASSIFICATION:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
  FILING DATE: 07-JUN-1995
CLASTELEGATION:
TELECOMMUNICATION INFORMATION:
TELEPRAX: 202-371-260
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTER.ESTICS:
LENGTH: 25 base pairs
TYPE: mucleic acid
STRANDEDNESS: both
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                25; Conservative
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STRANDEDNESS: both
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Best Local Similarity
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US-09-432-085-16
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APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Hartley, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT PILING DATE: 2002-11-21
FURNERT FILING DATE: 2002-11-21
PRIOR PLILOR INVENTION NUMBER: US/09/907, 719
PRIOR PLILOR DATE: 1998-110-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
SSOFTWARE: Patentin Ver. 2.0
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US-09-965-448-16

US-09-965-448-16

Sequence 16, Application US/09985448

Publication No. US20030157716A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Temple, Gary F.

APPLICANT: WORNER: US COMPINER: US CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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US-09-985-448-16
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Length 25;
Query Match
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0;
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Gaps
Gaps
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APPLICANT: Hartley, James L.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
Recombination Sites
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
PRIOR APPLICATION NUMBER: US/10/058,292
FILING DATE: 30-Jan-2002
CLASSIFICATION: CURROWN>
PRIOR APPLICATION: CURROWN>
PRIOR APPLICATION: APPLICATION OWNER: 09/432,085
FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JAN-1998
  Indels
                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX,
STREET: 1100 New York Ave., N. W. Suite 600
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  Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 11:
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                                                                                     1 GTTCAGCTTTCTTGTACAAGTTGG 25
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COMPUTER READABLE FORM:
MEDIUM TYPE: F10Ppy disk
COMPUTER: IBM PC compatible
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APPLICANT: Hartley, James L.; Brasch, Michael A.
                                                                                                                                                                                      US-10-058-292-11
; Sequence 11, Application US/10058292
; Publication No. US20030054552A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
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                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 35
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  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 25; Conserv
                                           1 GTTCAGCT
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US-10-058-292-16
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    Matches
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US-10-055-001A-11

Sequence 11, Application US/10055001A

Publication No. US20030049835A1

Publication No. US20030049835A1

GENERAL INFORMATION:

APPLICANT: Wesley, Susan V.

APPLICANT: Wesley, Susan V.

APPLICANT: Wethod and means for producing efficient silencing constructs

TITLE OF INVENTION: Wethod and means for producing efficient silencing constructs

TITLE OF INVENTION: Using recombinational cloning

FILE REFERENCE: HELLGA

CURRENT APPLICATION NUMBER: US/10/055,001A

CURRENT FILING DATE: 2002-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.1

SEQ ID NO 11

TANNAMATION 11
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 6, Application US/10055001A

Sublication No. US2030049835A1

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Wesley, Susan V.
APPLICANT: Hellivell, Christopher A.
TITLE OF INVENTION: Weing recombinational cloning
FILE REFERENCE: HELLGA
CURRENT PALICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOGTWARE: Patentin version 3.1
LENGTH: 25
LENGTH: 25
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                                                                         Description of Unknown Organism: recombination
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                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                   DB 12;
                                                                                                                                                                                    0.05;
                                                                                                                                                                   100.0%; Score 25; DB ilarity 100.0%; Pred. No. 0.0 Conservative 0; Mismatches
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ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial sequence
                                                   FEATURE:
OTHER INFORMATION: Descripti
OTHER INFORMATION: products
US-10-300-892-16
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Best Local Similarity
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Best Local Similarity
Matches 25; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 25; Conserv
       TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-055-001A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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S-10-16.2-8,0-1.0
Sequence 16, Application US/10162879
Sequence 16, Application US.20030068799A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTY: USA
COUNTY: USA
COMPUTER: TO005-3934
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Floppy disk
COMPUTER: TOOPY disk
COMPUTER: TOOPEN: Floppy disk
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/162,879
FILING DATE: 6-Jun-2002
CLASSIFICATION: CURROWN>
PRIOR APPLICATION NUMBER: US/09/432,085
FILING DATE: CURROWN>
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 14; Length 25; 100.0%; Pred. No. 0.05; ive 0; Mismatches 0; Indels
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/162,879
FILING DATE: 06-Jun-2002
CLASSIFICATION: <a href="https://doi.org/10/162/979">https://doi.org/10/162/979</a>
                                                                                                                                                      PRILICATION NUMBER: US/09/432,085
FILING DATE: «Unknown)
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-7AN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-0AN-1999
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-UN-1996
TELECOMMUNICATION INFORMATION:
TELEPRAS: 202-371-260
INFORMATION FOR SEQ. ID NO: 11:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: DOCH

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-162-879-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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Best Local Similarity luv..
Best Local Similarity
Local Similarity
Local Similarity
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US-10-162-879-16
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APPLICANT: Hartley, James L.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
Recombination Sites
                        TITLE OF INVENTION: Recombinational Cloning Using Engineered Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET 1100 New York Ave., N. W. Suite 600
CITY: Mashington
STATE: DC
                                                                        NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 14; Length 25; 100.0%; Pred. No. 0.05;
                                                                                                                                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: TEM PC COMPATIBLE

COMPUTER: TEM PC COMPATIBLE

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/058,292

FILING DATE: 30-47an-2002

CLASSIFICATION: CUNKNOWN>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/432,085

FILING DATE: 1999-11-02

APPLICATION NUMBER: 09/23,493

FILING DATE: 1999-11-02

APPLICATION NUMBER: 09/05,476

FILING DATE: 07-47N-1999

APPLICATION NUMBER: 08/63,002

FILING DATE: 07-47N-1999

APPLICATION NUMBER: 08/663,002

FILING DATE: 07-47N-1999

FILING DATE: 07-47N-1999

FILING DATE: 07-47N-1999

FILING DATE: 07-47N-1999

FILING DATE: 07-47N-1996

APPLICATION NUMBER: 08/486,139

FILING DATE: 07-47N-1995
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
CMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-058-292-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TGTACAAAGTTGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gricagcrircriciacaaagridg 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 11, Application US/10162879 Publication No. US20030068799A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                   COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-162-879-11
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Gaps

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Sequence 10. Application US/09732914

Fatent No. US20020007051A1

GENERAL INFORMATION:

APPLICANT: Cheo, David

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Heaven.

TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in TITLE OF INVENTION: Recombinational Cloning

FILE REFERENCE: 0942.501002

CURRENT FILNG DATE: 2000-12-10

FRIOR APPLICATION NUMBER: US 60/169,983

FRIOR APPLICATION NUMBER: US 60/188,020

FRIOR APPLICATION NUMBER: US 60/188,020

FRIOR PRILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 140

SEQ ID NO 10

SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.05;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 9; Length 27;
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has 0; Indels
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100.0%; Pred. No. 0.051;
tive 0; Mismatches 0; Indels
            APPLICANT: Fleming, Elena
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE COF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 24601-420
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 56
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GTTCAGCTTTCTTGTACAAAGTTGG 25
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; Sequence 34, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; OTHER INFORMATION: attP2, P3
US-10-161-403-56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25; Conservative
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Matches 25; Conserva
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US-09-732-914-10
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                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 14; Length 25; 100.0%; Pred. No. 0.05; ative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Perez, Carl
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Leung, Josephine
APPLICANT: Fleming, Elena
APPLICANT: Fleming, Elena
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE OF THING THE : 2001-05-05
CURRENT APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-05-31
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SECTUMARE: FASLSEQ for Windows Version 4.0
                                                                                                                                                                                                                                             TOPOLOGY: both

MOLECULE TYPE: CDNA
US-10-162-879-16
APPLICATION NUMBER: 08/486,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTTCAGCTTTCTTGTACAAAGTTGG 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GricaGciricirciacaagried 25
               FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 56, Application US/10161403
Publication No. US20030119104A1
GENERAL INFORMATION:
APPLICANT: Perkins, Edward
APPLICANT: Perez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Greene, Amy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 51, Application US/10161403
Publication No. US20030119104A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; OTHER INFORMATION: attR3 US-10-161-403-51
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US-10-161-403-56
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APPLICANT: LI, XIAO
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: BESOSITO, DOMINIC
APPLICANT: BYRD, DEVON R.N.
TITLE OF INTENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI FILE REFERENCE: 0942.5120001
FURRENT APPLICATION NUMBER: US/10/151,690
FURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 10/151,690
APPLICANT: LI, XIAO
APPLICANT: ESCOSITO, DOMINIC
APPLICANT: BYRD, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
FILE REFERENCE: 0942-5120001
FILE REFERENCE: 0942-5120001
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 10/151,690
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR PILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SEQ ID NOS: 64
SEQ ID NO 21
ENGTH: 4470
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OTHER INFORMATION: plasmid pDONR201
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Publication No. US20030124555A1
GENERAL INFORMATION
APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: gene
COCATION: (656)..(961)
OTHER INFORMATION: ccdB
FEATURE:
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; LOCATION: (3495)..(4134)
; OTHER INFORMATION: ori
US-10-151-690-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: gene
LOCATION: (2210)..(2442)
OTHER INFORMATION: attP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: gene
LOCATION: (29)..(260)
OTHER INFORMATION: attPl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: gene
LOCATION: (1303)..(1962)
OTHER INFORMATION: CMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: gene
LOCATION: (2565)..(3374)
OTHER INFORMATION: Kmr
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LOCATION: (1099)..(1184)
OTHER INFORMATION: ccdA
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US-10-151-690-63
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APPLICANT: CHEO, DAVID
APPLICANT: CHEO, DAVID
APPLICANT: CHEO, DAVID
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: ESPOSITO, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOL
CURRENT APPLICATION NUMBER: US/10/151,690
CURRENT APPLICATION NUMBER: US 10/151,690
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR FILING DATE: 2002-05-21
PRIOR FILING DATE: 2001-06-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
                                                                                                       TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOLY CURRENT APPLICATION NUMBER: US/10/151,690

CURRENT APPLICATION NUMBER: US 10/151,690

PRIOR APPLICATION NUMBER: US 00/2-05-21

PRIOR PILING DATE: 2002-05-21

PRIOR PLICATION NUMBER: US 60/291,973

PRIOR PILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 64

SOFTWARE: Patentin version 3.1

SEQ ID NO 34

LENGTH: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.0%; Score 25; DB 14; Length 27; Best Local Similarity 100.0%; Pred. No. 0.051; Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE: OTHER INFORMATION: plasmid pDONR212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 20
US-10-151-690-21
US-10-151-690-21
; Pacquence 21, Application US/10151690
; Publication No. US20030124555A1
; GENERAL INFORMATION
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 62, Application US/10151690 Publication No. US20030124555A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Artificial sequence
                                    LI, XIAO
ESPOSITO, DOMINIC
BYRD, DEVON R.N.
                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: attP2
US-10-151-690-34
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LENGTH: 4428
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                                                             APPLICANT: APPLICANT:
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Sequence 23, Application US/10055001A

Subjication No. US20030049835A1

Subjication No. US20030049835A1

GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Wesley, Peter
APPLICANT: Weterhouse, Peterhouse, Peterho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Waing recombinational cloning
FITLE OF INVENTION: Using recombinational cloning
FITLE OF INVENTION: Using recombinational cloning
FITLE OF INVENTION: Using recombinational cloning
FURENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 17862
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100.0%; Score 25; DB 14; Length 17862;
Best Local Similarity 100.0%; Pred. No. 0.16;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
100.0%; Score 25; DB 14; Length 5584;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14520 GTTCAGCTTTCTTGTACAAGTTGG 14544
PRIOR APPLICATION NUMBER: US 10/151,690
PRIOR FILING DATE: 2002-05-21
PRIOR PILING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
SEQ ID NO 61
LENGTH: 5584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 23, Application US/10055001A Publication No. US20030049835Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: plasmid pDONR207
US-10-151-690-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial sequence
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US-10-055-001A-23/c
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US-10-055-001A-23
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APPLICANT: BESOGITO, DOMINIC
APPLICANT: BSPOGITO, DOMINIC
APPLICANT: BYED, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
FILE REFERENCE: 0942.5120001
CURRENT PELLICATION NUMBER: US/10/151,690
CURRENT FILING DATE: 2002-05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: BRASCH, MICHAEL A.
APPLICANT: HENO, DAVID
APPLICANT: LI, XIAO
APPLICANT: BSPOSITO, DOMINIC
APPLICANT: BSPOSITO, DOMINIC
APPLICANT: BYEN, DEVON R.N.
IIILE OF INVENTIONS COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOL
FILE REPERENCE: 0942.5120001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 25; DB 14;
Best Local Similarity 100.0%; Pred. No. 0.13;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/10/151,690
CURRENT FILING DATE: 2002-05-21
PRIOR FILINGTATION NUMBER: US 10/151,690
PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
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                                                60/291,973
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US-10-151-690-64
                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: plasmid pDONR212
US-10-151-690-63
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Publication No. US20030124555A1
GENERAL INFORMATION:
APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 64, Application US/10151690
Publication No. US20030124555A1
GENERAL INFORMATION:
   PRIOR FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: Patentin version 3.1
SEQ ID NO 63
LENGTH: 4627
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                                                                                                                                                                                                                                                                                             ORGANISM: Artificial sequence
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Best Local Similarity 100.0
Matches 25; Conservative
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US-10-151-690-61/c
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                                                                                                                                                                                                                                                               TYPE: DNA
                                                                                                                                                                                                                                                                                                                                       FEATURE:
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RESULT 27
US-10-055-01A-13/C
US-10-055-01A-13/C
Sequence 13, Application US/10055001A
Publication No. US2030049835A1
GENERAL INFORMATION:
PAPLICANT: Wesley, Susan V.
APPLICANT: Wetley, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Wethod and means for producing efficient silencing constructs
TITLE OF INVENTION: Using recombinational cloning
FILE REFERENCE: HELLGA
CURRENT PELLIKG DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: ParentIn version 3.1
SEQ ID NO 13
LENGTH: 18691
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Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (17922)..(18687)
OTHER INFORMATION: octopine synthase gene terminator region
LOCATION: (13675)..(13980)
OTHER INFORMATION: ccdB selection marker (complement)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
NAMPKEY: misc feature
LOCATION: (1443)...(2148)
OTHER INFORMATION: nopaline synthase gene terminator
FEATURE:
                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (264)..(496)
OTHER INFORMATION: nopaline synthase gene promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KE: misc_feature
LOCATION: (10706)..(11324)
OCHER INFORMATION: right T-DNA border fragment
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature
i_LOCATION: (2149)..(2706)
cother INFORMATION: a left T-DNA border region
US-10-055-001A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: acceptor vector PHELLSGATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (11674)..(13019)
OTHER INFORMATION: CaMV35S promoter fragment
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: (7922)..(9985)
OTHER INFORMATION: spectinomycin resistance
                                                                                                  NAME/KEY: misc feature
LOCATION: (13048)..(13279)
OTHER INFORMATION: attP1 recombination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14520 GTTCAGCTTTCTGTACAAAGTTGG 14544
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                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (497)...(1442)
OTHER INFORMATION: nptII coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (17890)..(17659)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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FURDICACE 13, Application US/10055001A

FURDICACE 13. Application No. US20030049835A1

GENERAL INFORMATION:

APPLICANT: Wesley, Susan V.

APPLICANT: Wesley, Susan V.

TITLE OF INVENTION: Method and means for producing efficient silencing constructs

TITLE OF INVENTION: Wethod and means for producing efficient silencing constructs

TITLE OF INVENTION: Without a combinational cloning

FILE REFERENCE: HELICAA

CURRENT APPLICATION NUMBER: US/10/055,001A

CURRENT FILING DATE: 2002-06-11

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 13

LENGTH: 18691
                                                                                                                                                                                                                0;
                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                0;
                                                                                                                                                       Query Match 100.0%; Score 25; DB 14; Length 17862; Best Local Similarity 100.0%; Pred. No. 0.16; Matches 25; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (16551)..(16319)

THER INFORMATION: attP2 recombination site (complement)
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LOCATION: (17890)..(17659)
DTHER INFORMATION: attP1 recombination site (complement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc feature
LOCATION: (17610)..(16855)
OTHER INFORMATION: codB selection marker (complement)
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LOCATION: (15002)..(15661)
OTHER INFORMATION: chloramphenicol resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (10706)..(11324)
OTHER INFORMATION: right T-DNA border fragment
                                                                            ; OTHER INFORMATION: acceptor vector pHELLSGATE4
US-10-055-001A-23
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NAME/KEY: misc_feature
LOCATION: (11674)..(13019)
OTHER INFORMATION: CaMV35S promoter fragment
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LOCATION: (14387)..(14619)
OTHER INFORMATION: attP2 recombination site
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LOCATION: (7922)..(9985)
OTHER INFORMATION: spectinomycin resistance
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LOCATION: (14660)..(16258)
OTHER INFORMATION: pdk2 intron
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                              ORGANISM: Artificial sequence
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NAME/KEY: misc_feature
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US-10-055-001A-13
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Sequence 43, Application US/09907900

Fatent No. US2020212293A1

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REPERBNCE: 0942.2860004
CURRENT FILING DATE: 201-07-19
PRIOR PELLING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 43

LENGTH. 25
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Publication No. US20020192819A1
Publication No. US20020192819A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having;
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Unknown PERTURE: OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: Description of Unknown Organism: recombination; OTHER INFORMATION: products
US-09-855-797A-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95.2%; Score 23.8; DB 9; Length 25; llarity 88.0%; Pred. No. 0.18; Conservative 3; Mismatches 0; Indels
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CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/296,281
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SEQ ID NO 43
LENGTH: 25
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Best Local Similarity
Matches 22; Conserv
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ORGANISM: Unknown
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NAME/KEY: misc_feature
LOCATION: (17922)..(18687)
OTHER INFORMATION: octopine synthase gene terminator region
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Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                      LOCATION: (16551)..(16319)
OTHER INFORMATION: attP2 recombination site (complement)
                       OTHER INFORMATION: attPl recombination site (complement)
                                                                                 WAME/KEY: misc feature
LOCATION: (176T0)..(16855)
OTHER INFORMATION: ccdB selection marker (complement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc feature
LOCATION: (13675)..(13980)
OTHER INFORMATION: ccdB selection marker (complement)
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LOCATION: (1443)..(2148)
OTHER INFORMATION: nopaline synthase gene terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: wisc feature
LOCATION: (264)..(496)
OTHER INFORMATION: nopaline synthase gene promoter
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LOCATION: (15002)..(15661)
OTHER INFORMATION: chloramphenicol resistance gene
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LOCATION: (2149)..(2706)

CIHER INFORMATION: a left T-DNA border region

US-10-055-001A-13
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LOCATION: (13048)..(13279)
OTHER INFORMATION: attR1 recombination site
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LOCATION: (14387)..(14619)
OTHER INFORMATION: attP2 recombination site
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LOCATION: (497)...(1442)
OTHER INFORMATION: nptII coding region
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LOCATION: (14660)..(16258)
THEER INFORMATION: pdk2 intron 2
                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (16551) .(163
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NAME/KEY:
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FILE REFERENCE: 0942.2850004
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US-09-907-900-15
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APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/09/985,448
CURRENT FILING DATE: 1909-10-23
FRIOR FILING DATE: 1998-10-23
FRIOR FILING DATE: 1998-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PALENTION OF SEQ ID NOS: 60
SOFTWARE: PALENTION OF 3.
LENGTH: 25
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APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
IIILE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                             Gaps
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US-09-985-448-43
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US-09-907-719-43
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Pred. No. 0.18;
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Best Local Similarity 88.0%; Pred. No. 0.18;
Matches 22; Conservative 3; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3; Mismatches
CURRENT APPLICATION NUMBER: US/09/907,719
CURRENT FILING DATE: 2001-07-19
PRIOR PILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 43
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Sequence 43, Application US/09985448
; Publication No. US20030157716A1
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1 Similarity 88.0%;
22; Conservative
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Best Local Similarity
Matches 22; Conserv
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ORGANISM: Unknown
                                                                                                                                                                          TYPE: DNA
ORGANISM: Unknown
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US-09-985-448-43
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APPLICANT: Barach, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombination Sites
FILE REPERENCE: 0942.2850008
CURRENT APPLICATION NUMBER: US/09/855,797A
CURRENT FILING DATE: 1099-04-22
PRIOR PLING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: US 60/065,930
PRIOR PLING DATE: 1999-04-22
NUMBER OF SEQ ID NOS: 60
SSOTIMARE: PatentIn Ver. 2.0
SSOTIMARE: PatentIn Ver. 2.0
SSOTIMARE: PatentIn Ver. 2.0
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US-10-300-892-43
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Pred. No. 0.18;
3; Mismatches 0;
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Pred. No. 0.28;
0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/10/300,892
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/907,719
PRIOR FILING DATE: 2001-07-19
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SEQ ID NO 43
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Patent No. US20020094574A1
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; Patent No. US20020172997A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          95.2%;
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Best Local Similarity 96.0.
Thes 24; Conservative
                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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ORGANISM: Unknown
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ORGANISM: Unknown
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NUMBER OF SEQUENCES:
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Sequence 15, Application US/09907719

Publication No. US20020192819A1

GENERAL INFORMATION:

APPLICANT: Brasch, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Fox, Donna K.

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.2850004

CURRENT APPLICATION NUMBER: US/09/17, 19

CURRENT FILING DATE: 2001.07-19

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
APPLICANT: Fox, Donna K.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
FITLE OF INVENTION: Recombination Sites
FILE REPERBUCE: 0942.2856004
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/177,387
PRIOR APPLICATION NUMBER: 09/177,387
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 25
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7 OTHER INFORMATION: Description of Unknown Organism: recombination
7 OTHER INFORMATION: products
US-09-907-719-15
                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
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; Publication No. US20030100110A1
; GENERAL INFORMATION:
; APPLICANT: Bratch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
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96.0%; Pred. No. 0.28;
iive 0; Mismatches 1;
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Matches 24; Conservative
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                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Unknown
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US-09-432-085-15
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LENGIH: 25
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APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/09/985,448
CURRENT FILING DATE: 1999-110-23
FRIOR PRILING DATE: 1999-110-23
FRIOR APPLICATION NUMBER: US 60/065,930
FRIOR APPLICATION NUMBER: US 60/065,930
FRIOR FILING DATE: 1997-110-24
NUMBER OF SEQ ID NOS: 60
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                                                                                                                        COUNTRY: USA
ZIP: 20005-3334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
FILING DATE: (Herewith)
CLASSIFICATION:
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ilarity 96.0%; Pred. No. 0.28;
Conservative 0; Mismatches 1;
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEDUNDER: APPLICATION:
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER,
STREET: 1100 New York Ave.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25 base pairs
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Matches 24; Conserv
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TYPE: DNA ORGANISM: Artificial sequence
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STRANDEDNESS: both
                                                                                                                                                        Query Match 93.6%;
Best Local Similarity 96.0%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE,
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Best Local Similarity
Matches 24; Conserva
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LENGTH: 25
                                                                      FEATURE:
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APPLICANT: Wealey, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE OF INVENTION: using recombinational cloning
FILE REPERENCE: HELIGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT APPLICATION NUMBER: US/10/055,001A
SOFFRENT FILING DATE: 2002-06-11
SOFFWARE: Patentin version 3.1
SEQ ID NO 10
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US-10-300-892-15
Sequence 15, Application US/10300892
Publication No. US20030175970A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Tox, Donna K.
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT PILING DATE: 2002-11-21
PRIOR PLILING DATE: 2002-11-21
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATCHIN UNBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SEQ ID NO 15
LEMBET APPLICATION NUMBER: US/09/177,287
MANDER OF SEQ ID NOS: 60
SEQ ID NO 15
TEMPLE APPLICATION NUMBER: US/09/177,287
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CRGANICM: Unknown
EEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
                                                                                                                                     CTHER INFORMATION: Description of Unknown Organism: recombination in Other Information: products
US-09-985-448-15
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                                                                                                                                                                                                                                 Score 23.4; DB 12;
Pred. No. 0.28;
                                                                                                                                                                                                                                                                                    0; Mismatches
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GENERAL INFORMATION:
                                                                                                                                                                                                                                      Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative
  SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 25
                                                                             TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 39
US-10-055-001A-10
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                                                                                                                           FEATURE:
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GENERAL INFORMATION:
GENERAL INFORMATION:
Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
Recombination Sites
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Pred. No. 0.28;
0; Mismatches 1; Indels 0
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) OTHER INFORMATION: core sequence of recombination site attP1 US-10-055-001A-10
                                                           Length
                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
                                                             14;
                                                                                                   1;
                                                         Score 23.4; DB
Pred. No. 0.28;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/058,292
FILING DATE: 30-Jan-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/432,085
FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-07AN-1999
APPLICATION NUMBER: 09/05,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 09/663,002
FILING DATE: 07-UIN-1996
APPLICATION NUMBER: 08/486,139
APPLICATION NUMBER: 08/486,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: both
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GITCAGCTITCTIGIACAAGTIGG 25
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TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                US-10-058-292-15
; Sequence 15, Application US/10058292
; Publication No. US20030054552A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 202-371-2600
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OSTF163A3 OSTF177G3 OSTF162H1 OSTF202B1 OSTF099E7 OSTF137H4 OSTF163B1 OSTF175B7

Title: Perfect score:

Sequence:

nucleic

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Run on:

Scoring table:

Searched:

Minimum DB ( Maximum DB (

Database :

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CB388456 OSTF099E7
CB38444 OSTR137H4
CB394444 OSTR137H4
CB402012 OSTF205B3
CB400382 OSTF175B7
CB400130 OSTF169C5
CB400120 OSTF169C5
CB400120 OSTF11D4
CB401884 OSTF121D6
CB40120 OSTF11D5
CB40120 OSTF165C5
CB40120 OSTF166C5
CB398923 OSTF166C5
CB395B90 OSTF163A3
CB395B90 OSTR163A3
B1174863 OSTF061E9
                                                                                                                                                                                                                                                                                                                       BII74961 OSTFOGLE
BII74378 OSTFOGLE1
BII74378 OSTFOGLE1
BII74868 OSTFOGLD7
BII74892 OSTFOGLD7
BII74994 OSTFOGLD9
BII74910 OSTFOGLD1
CB960041 AGENCOURT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CB400039 87 bp mRNA linear EST 15-WAY-2003
OSTEL67D8 1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.
CB400039
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1 (bases 1 to 87)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li,S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Hualb, R., Chonce, M.R., Lee, H.,

C. elegans ORFeome version 1.1: experimental verification of the
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AL514767 AL514767
AL513677 AL513677
AL514171 AL514171
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CD048261 AGENCOURT
AL515449 AL515449
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genome annotation and resource for proteome-scale protein
         CB401751
CB401179
CB402581
CB392051
CB400512
CB392040
CB401874
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
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Contact: Vidal M
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expression
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CB392047 OSTF163A1
CB402537 OSTF214C1
CB402408 OSTF212B6
                                                                                      6, 2003, 22:08:13 ; Search time 1093.75 Seconds (without alignments) 555.531 Million cell updates/sec
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            GenCore version 5.1.6 (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Caenorhabditis elegans
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Nat. Genet., (20
Contact: Vidal M
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Best Local Similarity
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Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Peloderinae, Caenorhabditis.

1 (bases 1 to 90)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, V.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptackk, J., Snyder, M., Hill, D.E. and Vidal, M. C. elegans Orkeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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OSTF163A10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB392047
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/dow stage="mixed stage"
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/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of gones by poly(A) priming. The
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Tel: 617 632 5739

Email: Marc Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Conteact david_hill@dfci.harvard.edu or
                Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
Sequence to predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
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                                                                                                                                                                              /organism="Caenorhabditis elegans"
/mol type="mRNA"
/strain="N2"
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/strain="N2"
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100.0%; Pre
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617 632 5739
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Contact: Vidal M
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ENKARYOCTE, METAZOZO, Nematoda, Chromadorea, Rhabditida, Rhabditoidea Rhabditidae, Peloderinae, Caenorhabditis.

(Rabbditidae, Peloderinae, Caenorhabditis.

(Bases 1 to 92)

(Bases 1 to 92)

(C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Bartin,A., Tondenhaute,J., Boulton,S., Pracek,J., Jenna,S., Chevet,B., Papasotiropoulos,V., Tolias,P.P.

(Doucette-Stamm,L., Hill,D.E. and Vidal,M.

(C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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OSTF214C1 1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB402537
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/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into ppc86"
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1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Tel: 617 632 5739
Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
clouding project: Contact david_hill@dfci.harvard.edu
marc_vidal@dfci.harvard.edu
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//dev stage="mixed stage"
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//once="The AD-wrmcDNA"
// note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPCG6"

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100.0%; Pred. No. 24;
iive 0; Mismatches 0;
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Fri Nov

25

4 CAGCITICITGIACAAAGIIGG

à

Query Match
Best Local Similarity 100.
Matches 22; Conservative

32 CAGCTTTCTTGTACAAAGTTGG 11

RESULT 4 CB402408/c DEFINITION

LOCUS

Caenorhabditis elegans Caenorhabditis elegans

ORGANISM

AUTHORS

REFERENCE

ACCESSION VERSION

KEYWORDS

SOURCE

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Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 95)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson
                                                                                                                                                                         Enkaryotta, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea Bukaryotta, Metazoa, Nematoda, Caenorhabditis.

1 (bases 1 to 95)

1 (bases 1 to 95)

1 (bases 1 to 95)

2 (M. Li,S. Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.,F., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Brace,J., Jensa,S., Chevet,E., Papasotiropoulos,V., Tolias,P.D., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H., Doucette-Stamm,L., Hill,D.E. and Vidal,M.

C. elegans ORFeene version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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CB400591 95 bp mRNA linear EST 15-MAY-2003
OSTF17957_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Fax: 617 632 5739
Fax: 617 632 5739
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project: Contact david—inl@dfci.harvard.edu
marc_vidal@dfci.harvard.edu
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into ppCBs"
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Contact: Vidal M
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C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
                                                                                                                                                                                                                                                                                  94 bp mRNA linear EST 15-MAY-2003 OSTF212B6_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence. CB402408
CB402408.1 GI:30744135
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RNA isolated from both hermaphrodite and male N2 worms of
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subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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1 (bases 1 to 94)
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1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
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Location/Qualifiers

source

FEATURES

Nat. Genet., (2003) ] Contact: Vidal M Marc Vidal Laboratory

expression

JOURNAL

COMMENT

TITLE

4 CAGCITICITGIACAAAGIIGG 25

100.0%;

Query Match Best Local Similarity 100.

BASE COUNT ORIGIN

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RESULT 5 CB400591/c

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Eukaryotta, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea Bukaryotta, Metazoa, Nematoda, Chromadorea, Rhabditidae, Peloderinae, Caenorhabditis.

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Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotoc, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

G. elegans ORReame version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were
Sequence to Gateway entry clones. The primers of Gateway entry
Gesigned on the predicted protein encoding ORF. C. elegans ORFeome
designed on the predicted javid hill@dfci.harvard.edu or
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
CDNAs were cloned into pPC86"
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115,
Fax: 617 632 5180
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Contact: Vidal M
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Enkaryota, Metazoa, Nematoda, Chromadorea, Rhabditida; Rhabditoidea
1 (basea) to 97)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, M., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Braces, J., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M. Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.B. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
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OSTF190A5_1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.
                                               Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Pracek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, J., Hill, D.B. and Vidal, M. C. elegans ORPeome, varion 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
                                                                                                                                                                                                                                                           Marc Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5739

Email: Marc Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFecome
cloning project : Contact david_hill@dfci.harvard.edu
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Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
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/tissue_type="whole animal"
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/strain="N2"
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Contact: Vidal M
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidea; Peloderinae; Caenorhabditis.

1 (bases 1 to 100)
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
Doucctte-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORFsome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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Dana Farber Cancer Institute
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc-Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
POLYA=NO.
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RNA isolated from both hermaphrodite and male N2 worms of
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

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                                                         DB 14; Length 100;
25;
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Contact: Vidal M
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/strain="N2"
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/sex="Hermaphrodite and male"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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(Rases 1 to 100)

Reboul, J., Vaglio, P., Rual, J. F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vadenhaute, J., Boulton, S., Pracek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M. C. elegans ORFeame version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc vidal@dfci.harvard.edu
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Contact: Vidal Marc Vidal Barc Vidal Barc Vidal Barca Total Training

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
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/mol type="mRNA"
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/Bex="Hermaphrodite and male"
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Matches 22; Conservative 0; Mismatches
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Fax: 617 632 5739
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Caenorhabditis elegans
Enkaryota, Metazoa: Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
l Chaes 1 to 107)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bartin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Bartin, N., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Pacckk, J., Snyder, M., Hill, D.E. and Vidal, M. C. elegans OrRecew version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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OSTF099E7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB388456
C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.T., Harley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Bndress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H., Doucette-Stamm,L., Hill,D.B. and Vidal,M.
C. elegans ORReome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
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cloning project: Contact david_hill@dfci.harvard.edu
marc_vidal@dfci.harvard.edu
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/tissue type="whole animal"
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/dev_stage="mixed stage"
/clone_lib="Ab-wrmcDNA"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
CDNAs were cloned into pPC86"
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/mol_type="mRNA"

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Contact: Vidal M
Marc Vidal Laboratory
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// Strath="wa"
// Sara="taxon:6239"
// Sax="Hermaphrodite and male"
// Lissue_type="whole animal"
// dev_gatage="mixed stage"
// dow_gatage="mixed stage"
// clone lib="AD-wrmcDNA"
// note="The AD-wrmcDNA library was generated with poly(A) +
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
31 a 14 c 22 g 35 t
                                                                                                                                                                                        Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 122)
Reboul,J.; Vaglio,P.; Rual,J.F.; Lamesch,P.; Martinez,M.; Armstrong,C.M.; Li,S.; Jacotch,L.; Bertin,N.; Janky,R.; Moore,T.; Hudson,J.R.; Hartley,J.L.; Brasch,M.A.; Vandenhaute,J.; Boulton,S.; Endress,G.A.; Johna,S.; Chevet,E.; Papasotiropoulos,V.; Tolias,P.P.; Pracek,J.; Snyder,M.; Hance,M.R.; Lee,H.;
C. elegans ORFeome version 1.1: experimental verification of the
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; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 103)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong
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                      CB392040 102 bp mRNA linear EST 15-MAY-2003
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Dana Farber Cancer Institute
Dana Farber Cancer Institute
Dana Farber Cancer Institute
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact david_hill@dfci.harvard.edu or
POLYÄ=NO.
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Pred. No. 25;
0; Mismatches 0; Indels
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/strain="N2"
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Contact: Vidal M
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Nat. Genet., (20
Contact: Vidal M
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CB402012/c
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                                                                                                                                                                                                                                            /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="No.
/strain="No.
/db xref="taxon:6239"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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C. elegans ORFsemmer version 1.: experimental verification of the genome annotation and resource for proteome-scale protein
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Caenorhabditis elegans
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
F. Rhabditidae; Peloderinae; Caenorhabditis.
Chases I to 111)
Chases I to 111)
Chases I to 111
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OSTR137H4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
1 Jimmy Fund had be a size of the primers used were Sequence tag of Gateway entry clones. The primers used were Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome designed on the contact david_hill@dfci.harvard.edu or
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
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Fax: 617 632 5739
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Contact. Vidal M
Marc Vidal Laboratory
Dana Faxber Cancer Institute
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marc_vidal@dfci.harvard.edu
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organism="Caenorhabditis elegans"

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l (bases 1 to 114)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacoto, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORPeene version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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OSTESSB3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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; Rhabditidae; Peloderinae; Caenorhabditis.
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Dana Farber Cancer Institute

La Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5180

Fax: 617 632 5739

Email: Marc Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact david hill@dfci.harvard.edu or
POLYÃ-NO.
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
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CDNAs were cloned into pPC86"
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/dev_Erge="whole animal"
/dev_Erge="whole animal"
/dev_Erge="missed stage"
/clone_lib="Ab-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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/organism="Caenorhabditis elegans"
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/strain="N2"
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Query Match

Best Loc Matches

BASE COUNT

ORIGIN

LOCUS

ACCESSION VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

CB392055/c

RESULT 16

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Caenorhabditis elegans
Caenorhabditis elegans
Caenorhabditis elegans
Caenorhabditis elegans
Bukaryota, Metazoa Nematoda; Chromadorea; Rhabditida; Rhabditoidea
Eukaryota, Metazoa Nematoda; Caenorhabditis.

[ (bases I to 120)
I (bases I to 120)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Pracek, J., Snyder, M., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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Caenorhabditis elegans
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 124)
                                                CB400382 12-MAY-2003
OSTF175B7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
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/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA library was generated with poly(A)+
/note="The AD-wrmcDNA library was generated with
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115,
Fax: 617 632 5180

    120
    organism="Caenorhabditis elegans"

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Contact: Vidal M
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 8E8, BOSTON, MA 02115, USA
Tel: 617 632 5739
Email: Narc Vidaladfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david hill@dfci.harvard.edu or
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/sex="Hermaphrodite and male"
/tissue type="whole animal"
/tissue type="mixed stage"
/dev_stage="mixed stage"
/clone lib="Ab-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
CDNAs were cloned into ppc86"
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100.0%; Pred. No. 26;
ive 0; Mismatches 0; Indels
                                                                                    14; Length 114;
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/mol_type="mRNA"
/strain="N2"
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29
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marc vidal@dfci.harvard.edu
POLYA=No.
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Contact: Vidal M
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Best\_Local Sim Matches 22; Query Match

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C. elegans ORFsome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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Caenorhabditis elegans
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 126)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotch, E., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M. A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Paceek, J., Snyder, M., Hudn, R., Chance, M.R., Lee, H., Constete-Stamm, L., Hill, D.E. and Vidal, M.
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                                                                                                                                                                                                                                                   Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund way Smith 858, BOSTON, MA 02115, USA
1 Jimmy Fund way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Faxil Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david hill@dfci.harvard.edu or
POLNÃ=NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tlssue_rype="mixed stage" dev_stage="mixed stage" dev_stage="mixed stage" /clone_lib="AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The CDNAs were cloned into pPC86"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Caenorhabditis elegans"
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/strain="N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Hermaphrodite and male"
/tissue_type="whole animal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   db_xref="taxon:6239"
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Best Local Similarity 100..
Best Local Similarity 20..
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Contact: Vidal M
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Contact: Vidal
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| Corganism="Caenorhabditis elegans" |
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Caenorhabditis elegans
Caenorhabditis elegans
Bukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea
1, Rhabditidae, Peloderinae, Caenorhabditis.
1 (bases I to 128)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Pacek, J., Snyder, M., Hill, D.E. and Vidal, M.
C. elegans Orrecene version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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OSTF171D4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
POLYA-NO.
                                                                                                                                                                           Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
POLYÄ-No.
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Fax: 617 632 5739
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
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Dana Farber Cancer Institute
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Contact: Vidal M
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Best Local Similarity
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Gaps

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Enkaryotes, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea Rhabditidae, Peloderinae, Caenorhabditis.

(bases i to 129)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Bracek, J., Snyder, M.A., Vandenhaute, J., Boulton, S., Pracek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
                                                                                                                                                                                                                                                                                                                CB401218 129 bp mRNA linear EST 15-MAY-2003
OSTF191C6_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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/clone lib="AD-wrmcDNA"
/clone="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC66"
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1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
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Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
cloup on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact david hill@dfci.harvard.edu or
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/mol_type="mRNA"
/strain="N2"
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cDNAs were cloned into pPC86"
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/tissue_type="whole animal"
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                                                                                                  100.0%; Pred. ... 0; Mismatches
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Pred. No.
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Caenorhabditis elegans
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Contact: Vidal M
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

1. (bases 1 to 128)
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Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Pacek, J., Snyder, M., Huall, D.E. and Vidal, M. C. elegans OrReame, V. Hill, D.E. and Vidal, M. C. elegans OrReame version 1.1: experimental verification of the genome annotation and resource for protecome-scale protein
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Fax: 617 632 5739
Bmail: Marc-Vidaledfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact david_hill@dfci.harvard.edu or
POLYA-No.
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/sex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
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OSTF202C5_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                        Score 22; DB 14; Length 128; Pred. No. 27;
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/organism="Caenorhabditis elegans"
        organism="Caenorhabditis elegans"
                                                               db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/tissue_type="whole animal"
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100.0%; Pred. No. ...
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/strain="N2"
                        type="mRNA"
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                                                strain=
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Contact: Vidal M
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us-10-055-001a-11.rst

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Eukaryotta, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea Rhabditidae, Peloderinae, Caenorhabditis.

Rhabditidae, Peloderinae, Caenorhabditis.

Robost, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Braces, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P. Pracek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Chocette-Stamm, L., Hill, D.E. and Vidal, M.

G. elegans ORFeene version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
                Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Bratess, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Pracek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M. C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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OSTR163A3_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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/tissue_type="whole animal"
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/note="The AD-wrmCDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

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Contact: Vidal M
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Dana Farber Cancer Institute

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Tel: 617 632 5139

Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu

marc_vidal@dfci.harvard.edu
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/strain="N2"
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Nat. Genet., (2003) In press
Contact: Vidal M
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Caenorhabditis elegans
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(bases 1 to 247)
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Caenorhabditis elegans

Eukaryota, Netazoa; Nematoda; Chromadorea; Rhabditida; Rhabditodea

Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 227)

1 (bases 1 to 227)

2 Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, M., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Pacette-Stamm, L., Hill, D.E. and Vidal, M. C. elegans ORFeome version 1.1: experimental verification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="N2"
/db.xef="taxon:6239"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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Caenorhabditis elegans
Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
? Rhabditidae; Peloderinae; Caenorhabditis.
                                                                      CB398923 227 bp mRNA linear EST 15-MAY-2003
OSTR21286_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 517 632 5139
Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project: Contact david_hill@dfci.harvard.edu
marc_vidal@dfci.harvard.edu
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/strain="N2"
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CB401020/c
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l. .263
/organism="Caenorhabditis elegans"
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Caenorhabditis elegans
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhadditidae; Peloderinae; Caenorhabditis.

I (bases 1 to 263)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Lis., Jaccott, J., Bertin, N., Janky, K., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Pracek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
C. elegans ORPenew version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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mRNA sequence.
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Tel: 617 632 5180
Fax: 617 632 5180
Fax: 617 632 5739
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                                                                                                                                                                                                         Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc vidal@dfci.harvard.edu
POLYA=No.
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Pred. No. 33;
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Marc Vidal Laboratory
Dana Farber Cancer Institute
I Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
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/mol_type="mRNA"
/strain="N2"
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100.0%; Pred. No. --.
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Dana Farber Cancer Institute
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                                                                                                                                  Tel: 617.632 5180
Fax: 617 632 5739
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Eukaryotta: Metazoza; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (Bases 1 to 380)
Reboul,J., Vaglio,P., Tzellas,N., Thierry-Mieg,N., Moore,T., Jackson,C., Shin-i,T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J., Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F., Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M. Open-reading-frame sequence tags (OSTS) support the existence of at least 17,300 genes in C. elegans
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OSTFO6IDB 1 AD-WIMCDNA Caenorhabditis elegans cDNA similar to
B1174869
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@dfci.harvard.edu or
philippe_vaglio@dfci.harvard.edu_
POLYA=No.
/sex="Hermaphrodite and male"
//tsue_type="whole animal"
//dev_grpe="whole animal"
//dev_grage="mixed stage"
//clone_lib="AD-wrmcDNA"
//note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of CDNAs by poly(A) priming. The
CDNAs were cloned into ppGG8"
a S1 C 84 9 B0 t
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/clone_lib="AD-wrmcDNA"
/clone_lib="AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
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Pred. No. 33;
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/organism="Caenorhabditis elegans"
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Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
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Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 435)
3 Ackson, C., Shin-1,T., Kohara,Y., Thierry-Mieg,N., Moore,T.,
Jackson,C., Shin-1,T., Kohara,Y., Thierry-Mieg,N., Thierry-Mieg,J.,
Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans
L Nat. Genet. 27 (3), 332-336 (2001)
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact jerome_reboul@dfci.harvard.edu or
philippe_vaglio@dfci.harvard.edu
POLYA=No.
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//tsue type="whole animal"
//dev stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/clone_lib="AD-wrmc
generation of CDNAs by poly(A) priming. The cloned into pPC86" 106 g 97 t
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                                                                                                                                                             DB 12; Length 380; 37;
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| strain="N2"
| db_xref="taxon:6239"
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Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
                                                                                                                                          Mismatches
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100.0%; Pre
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                                            cDNAs were
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Best Local Similarity
Matches 22; Conserv
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Caenorhabditis elegans
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases to 460)
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, J., Thierry-Mieg, J., Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M. Open-reading-frame sequence tags (OSTS) support the existence of at least 17,300 genes in C. elegans
Mat. Genet. 27 (3), 332-336 (2001)
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OSTFO61F9 1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to C45G7.2, mRNA sequence.
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Sequence tag Of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@dfci.harvard.edu or
PolINDe vaglio@dfci.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="AD-wrmcDNA".
/clone_lib="AD-wrmcDNA library was generated with poly(A)+
Note="The AD-wrmcDNA library was generated with poly(A)+
RNA islanded from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAS were cloned into pPCB6"

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Local Similarity 100.0%; Pred. No. 39;
Local Scince 100.0%; Pred. No. 39;
Local Scincervative 0; Mismatches 0; Indels
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/mol_type="mRNA"
/strain="N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Reboul J, Vaglio P
Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
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/tissue_type="whole animal"
/dev_stage="mixed stage"
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Caenorhabditis elegans
Caenorhabditis elegans
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KEYWORDS
SOURCE
ORGANISM
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REFERENCE

JOURNAL

COMMENT

TITLE

FEATURES

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Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
111 617 622 5180
Fax: 617 632 2425
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1 (bases 1 to 480)

1 (bases 1 to 480)

Thierry-Mieg,N., Moore,T.,
Jackson,C., Shin-1,T., Kohara,Y., Thierry-Mieg,N., Moore,T.,
Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)

11242119
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea , Rhabditidae, Peloderinae, Caenorhabditis.

(bass 1 to 467)

Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F., Open-reading-frame sequence tags (OSTs) support the existence of at
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/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
DNAs were cloned into pDC86"
a 87 c 101 g 126 t
                                                                                                                                                                                                                                                                                                                                                                     Email: Jerome Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact jerome_reboul@dfci.harvard.edu or
philippe_vaglio@dfci.harvard.edu
POLYA=NO.
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/mol_type="mRNA"
/strain="NZ"
                                                                                                                                                                                                                                                                     Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
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/sex="Hermaphrodite and male"
/tissue_type="whole animal"
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100.0%; Pred. No. 30,
0; Mismatches
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Genet. 27 (3), 332-336 (2001)
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Contact: Reboul J, Vaglio P
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Caenorhabditis elegans
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Best Local Similarity
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22; Conservative
                                                                                                                                                                     least 17,300
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BI174878
LOCUS
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VERSION KEYWORDS

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SOURCE

REFERENCE AUTHORS JOURNAL

TITLE

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/acamin_var
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/tisue_type="who.le animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA"
/note="The AD-wrmcD
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis;
1 (bases 1 to 501)
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Shin-!T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Diee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F., Prasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M. Open-reading-frame sequence tags (OSTS) support the existence of at least 17,300 genes in C. elegans
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@dfci.harvard.edu or
philippe_vagllo@dfci.harvard.edu
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORFeome
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Marc Vidal Laboratory
Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
17e1: 617 632 5180
Fax: 617 632 2425
Bmail: Jerome Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans Ol
cloning project : Contact jerome_reboul@dfci.harvard.edu or
pohilippe_vaglio@dfci.harvard.edu
Pohilippe_vaglio@dfci.harvard.edu
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88.0%; Score ___ 100.0%; Pred. No. 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
1. 549
                                                                                                                                                                              436 CAGCTTTCTTGTACAAAGTTGG 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CAGCTTTCTTGTACAAGTTGG 25
                                                                                                                                                        4 CAGCTTTCTTGTACAAGTTGG 25
                                                                                                                                                                                                                                                                                                                                         BI174892.1 GI:14640695
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                                                                                                                         22; Conservative
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Best Local Similarity 7
                                                                                          Query Match
Best Local Similarity
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                                           BASE COUNT
ORIGIN
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AUTHORS
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PUBMED
                                                                                                                           Matches
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BI174892
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                               Enkaryotta; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 508)
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T., Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, D., Thierry-Mieg, J., Brasch, M.A., Vandenhaute, J., Lamesch, P.E., Hill, D.E. and Vidal, M. Open-reading-frame sequence tags (OSTs) support the existence of at least 17, 300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         OSTF061D7_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to P28A10.3, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Jerome_Reboul@dfci.harvard.edu
Email: Jerome_Reboul@dfci.harvard.edu
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact jerome_reboul@dfci.harvard.edu or
philippe_vaglio@dfci.harvard.edu
POLYA=NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xxef="taxon:6239"
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/tissue_type="whole animal"
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/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
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0
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    508
    /organism="Caenorhabditis elegans"

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Dana Farber Cancer Institute

H Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180

Fax: 617 632 2425
                                                                                                                                                                                                                                                                                                               40;
                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                               Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                         453 CAGCTTTCTTGTACAAGTTGG 474
                                                                                                                                                                                                                                                                                                                                                               4 CAGCTTTCTTGTACAAGTTGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Reboul J, Vaglio P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="mRNA"
/strain="N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI174868.1 GI:14640671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Caenorhabditis elegans
Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                              22; Conservative
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Matches 22; Conserv
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ORIGIN
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PUBMED
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BI174868
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KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
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FEATURES
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Caenorhabditis elegans
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.
1 (bases 1 to 54)
Reboul,J., Vaglio,P., Tzellas,N., Thierry-Wieg,N., Moore,T.,
Jackson,C., Shin-i,T., Kohara,Y., Thierry-Mieg,D., Thierry-Mieg,J.,
Brasch,M.A., Vandenhaute,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
Open-reading-frame sequence tags (OSTS) support the existence of at
least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
                                                                                                                                                                                                                                                                                                                                                              OSTICATED SAP DE MRNA linear EST 09-JUL-2001
OSTICATED 1 AD-WIMCDNA Caenorhabditis elegans cDNA similar to
B1174892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
a 134 c 119 g 127 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"

102 c 105 g 180 t
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                                                                                                                                            Score 22; DB 12; Length 508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Caenorhabditis elegans"
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/strain="N2"
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 35

CB395875

ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

TITLE

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Caenorhabditis alegans
Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 613)
Reboul, J., Vaglio, P., Tzellas, N., Thierry-Mieg, N., Moore, T.,
Jackson, C., Shin-i, T., Kohara, Y., Thierry-Mieg, N., Thierry-Mieg, J.,
Lee, H., Hitti, J., Doucette-Stamm, L., Hartley, J.L., Temple, G.F.
Open-reading-frame sequence tags (OSTs) support the existence of at least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                613 bp mRNA linear EST 09-JUL-2001
OSTF062B7_1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to
B1174910
     Eukaryotta; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae, Peloderinae; Caenorhabditis.

1 (bases 1 to 583)
Reboul,J., Vaglio,P. Tzellas,N., Thierry-Mieg,N., Moore,T.,
Lee,H., Hitti,J., Doucette-Stamm,L., Hartley,J.L., Temple,G.F.,
Brasch,M.A., Vandenhaure,J., Lamesch,P.E., Hill,D.E. and Vidal,M.
Open-reading-frame sequence tags (OSTS) support the existence of at least 17,300 genes in C. elegans
Nat. Genet. 27 (3), 332-336 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Hermaphocite and male"
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/dev_stage="mixed_stage"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
a 158 c 109 g 124 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: Jerome Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans O
cloning project : Contact jerome_reboul@dfci.harvard.edu or
philippe_vaglio@dfci.harvard.edu
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100.0%; Pred. No. 42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Caenorhabditis elegans"
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/strain="N2"
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Dana Farber Cancer Institute
44 Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db xref="taxon:6239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  519 CAGCTTTCTTGTACAAAGTTGG 540
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                                                                                                                                                                                                                                                                                                                                 Contact: Reboul J, Vaglio P
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100.0%; Fic
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Caenorhabditis elegans
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ORIGIN
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BI174910
LOCUS
ORGANISM
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PUBMED
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                                                                           REFERENCE
                                                                                                      AUTHORS
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                                                                                                                                                                                                                                                                                                      Eukaryotta; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 559)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Budress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Chocette-Stamm, L., Hill, D.B. and Vidal, M. C. elegans ORFeome version 1.1: experimental verification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:6239"
/sex="Hermaphrodite and male"
/issue_type="whole animal"
/clone_tib="wap="mixed stage"
/clone_lib="wap="wncDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of CDNAs by poly(A) priming. The
CDNAs were cloned into ppC86"
a 120 c 113 g 163 t
                                                                                                                            559 bp mRNA linear EST 15-MAY-2003
Caenorhabditis elegans cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OSTF062B11 1 AD-wrmcDNA Caenorhabditis elegans cDNA similar to T06A4.2, mENA sequence.
B1174904
B174904.1 G1:14640707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Pred. No. 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expression.

Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Fax: 617 632 5739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
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     CAGCTTTCTTGTACAAGTTGG 498
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CB395875
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Caenorhabditis elegans
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Best Local S:
Matches 22
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source

FEATURES

BASE COUNT

ORIGIN

DEFINITION

RESULT 36

à

BI174904

ACCESSION

VERSION KEYWORDS SOURCE

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Gaps

Gaps

. 0

PUBMED

COMMENT

FEATURES

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/with a NotI-oligo(dT) primer. Five prime end enriched,
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
18 c 68 g 163 t 60 others
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                                                                                                                                                               /location in the many many contents and contents of the many contents of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 559)
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cgi-bin/cluster.cgi?seq=CLOBB019ZB04FPl&cluster=1606.r. Contact
Feng Liang Email: filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CLOBB019ZB04FPl.
Location/Qualifiers
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1606.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liwas. Gruber. C., Jessee, J. and Polayes, D.
Liwas., Gruber. C., Jessee, J. and normalization
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12778882.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 88.0%; Score 22; DB 14; Length 1388; Best Local Similarity 100.0%; Pred. No. 55; Matches 22; Conservative 0; Mismatches 0; Indels (
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/issue_type="Human Placenta"
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/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="CL0BB019ZB04"
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271 c 314 g
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Best Local Similarity
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KEYWORDS
SOURCE
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AL515389/c
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AUTHORS
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Email: cgapbs-r@mail.nib.gov

Tissue Procurement: Dr. Stefan Hansson
cDNA Library Preparation: Michael J. Brownstein (NHGRI) with help
and advice from Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: NDAMATI row: d column: 04
High quality sequence stat: 138
High quality sequence stop: 355.
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NIH-WGC http://mgc.nci.nih.gov/.
                                                                                                                                                                                                                                                                                                                                   Email: Jerome Reboul@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact jerome_reboul@dfci.harvard.edu or
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AGENCOURT 13887498 NIH MGC 147 Homo sapiens CDNA clone
IMAGE:30340779 5', mRNA sequence.
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Pred. No. 43;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Caenorhabditis elegans"
/wol_type="mRNA"
/strain="N2"
                                                                               Contact: Reboul J, Vaglio P
Marc Vidal Labbratory
Dana Farber Cancer Institute
Tels Binney Street, Boston, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 2425
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100.0%; Pred. No. --.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                philippe_vaglio@dfci.harvard.edu
POLYA=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        551 CAGCTTTCTTGTACAAGTTGG 572
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                                                                          Reboul J, Vaglio P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CB960041
CB960041.1 GI:30216157
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Matches 22; Conservative
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL COMMENT

FEATURES

LOCUS

ACCESSION

CB960041/c

RESULT 38

BASE COUNT ORIGIN

Fri Nov

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Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 982)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D.

Email: Gapbse-r@mail.nih.gov

Tissue Procurement: Dr. Jamie Thompson, University of WI

CONA Library Preparation: Gina Zastrow-Hayes

CDNA Library Preparation: Gina Zastrow-Hayes

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://mage.lln.gov

Plate: NDKM41 row: p column: 19

High quality sequence start: 11

High quality sequence start: 11

High quality sequence start: 11

High quality sequence story: 472.
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/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/tissue type="embryonic stem cell"
/tissue type="embryonic stem cell"
/tab host="DH10B TonA"
/clone llb="NHH MGC 172"
/note="Vector: pDONR201; Site 1: attP2; Site 2: attP1;
LIBR PRIMING - oligo dT; METHOD - full-length enriched;
Embryonic Stem Cells H1; LIBR PROVIDER - Bradfield"
03 a 198 c 219 g 146 t 216 others
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AGENCOURT_13971692 NIH_MGC_172 Homo sapiens cDNA 5', mRNA sequence.
  Gaps
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0; Mismatches
                                                 4 CAGCTTTCTTGTACAAGTTG 24
                                                                                             40 cagcrircirgracaaagrig 20
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21; Conservative
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                                                                                                                                                                 RESULT 40
CD048261
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AUTHORS
TITLE
JOURNAL
COMMENT
Matches
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Gaps

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Query Match

84.0%; Score 21; DB 14; Length 982;
Best Local Similarity 95.5%; Pred. No. 1.4e+02;
Matches 21; Conservative 0; Mismatches 1; Indels

Search completed: November 7, 2003, 00:21:01 Job time: 1094.75 secs

us-10-055-001a-10.rni

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TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-233-493-15
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US-09-233-493-15
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                                                                   6, 2003, 22:12:53 ; Search time 28 Seconds (without alignments) 394.092 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 43,
Sequence 11,
Sequence 16,
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Sequence 15,
Sequence 15,
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Sequence 15,
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Sequence 18,
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Sequence 1
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\(\lambda\text{Tina/SA_COMB.seq:*}\)
\(\lambda\text{Com2_6/ptodata/1/ina/SB_COMB.seq:*}\)
\(\lambda\text{Com2_6/ptodata/1/ina/6A_COMB.seq:*}\)
\(\lambda\text{Com2_6/ptodata/1/ina/BE_COMB.seq:*}\)
\(\lambda\text{Com2_6/ptodata/1/ina/BE_COMB.seq:*}\)
\(\lambda\text{Com2_6/ptodata/1/ina/PcTUS_COMB.seq:*}\)
\(\lambda\text{Com2_6/ptodata/1/ina/Packfiles1.seq:*}\)
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-005-476-15
US-09-296-280-15
US-09-296-280-15
US-09-498-074-15
PCT-US96-10082A-15
US-09-233-493-11
US-09-233-493-11
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US-09-233-493-11
US-09-233-493-11
US-09-233-492-11
US-09-233-492-11
US-09-233-492-11
US-09-296-280-16
US-09-296-280-16
US-09-296-16
US-09-498-074-11
US-09-498-074-11
US-09-498-074-16
US-09-498-074-16
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US-09-498-074-16
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US-09-296-280-42
US-08-021-667A-18
                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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US-09-233-492-9
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US-09-498-074-9
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                                                                                                                                                                                                   569978 seqs, 220691566 residues
                                                                                                                                          1 gttcagcttttttgtacaaagttgg 25
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                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                               - nucleic search, using sw model
                                                                                                                                                                  IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                 US-10-055-001A-10
25
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Match Length DB
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                                                                                                                      Title:
Perfect score:
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                                                                                                                                               Sequence:
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Sequence 15, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STERET: 1100 New York Ave., N. W. Suite 600
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: DC
COUNTRY: USA
ZID: 20005-3934
ZIP: 20005-3934
COMPUTER: EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PatentIN PC-DOS/MS-DOS
SOFTWARE: PatentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
US-08-728-785A-18
US-08-556-978B-78
US-07-559-98BA-1
US-09-233-493-10
US-09-233-492-10
US-09-296-280-11
US-09-296-280-11
US-09-296-280-11
US-09-33-493-12
US-09-33-493-14
US-09-233-493-14
                                                                                                                                                                                                                                                                                                          ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEPROMMUNICATION INFORMATION:
TELEPROMMUNICATION INFORMATION:
TELEPROMMUNICATION INFORMATION:
TELEPROMMUNICATION 170-2600
TELEFRAX: 202-371-2540
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APPLICANT: Hartley, James L.
APPLICANT: Hartley, Michael A.
APPLICANT: Barach, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.285007
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT APPLICATION NUMBER: US 09/117,387
EARLIER FILING DATE: 1999-04-22
EARLIER FILING DATE: 1998-10-23
EARLIER FILING DATE: 1998-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 15
LENGTH: 25
LENGTH: 25
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100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                             COMPUTER KEALABLE FORD

MEDITUM TYPE: FIDEPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PRICE PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/63,002
FILING DATE: 07-JUN-1996
CLASSIFICATION
PRIOR APPLICATION
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTTCAGCTTTTTTGTACAAGTTGG 25
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Patent No. 6277608
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.
Best Local Similarity 100.
Matches 25; Conservative
                              COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
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STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-296-280-15
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Sequence 15, Application US/09005476

Batent No. 6171861

GENERAL INFORMATION:

APPLICANT: Hariley, James L.

APPLICANT: Brasch, Michael A.

TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: 35

CORRESPONDENCES: 35

CORRESPONDENCES: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 New York Ave., N. W. Suite 600

CITT: Machington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 3; Length 25; 100.0%; Pred. No. 0.077; cive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: STENE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476 FILING DATE: herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | GTTCAGCTTTTTTGTACAAAGTTGG 25
                                                                                                                                     1 GITCAGCTITITIGIACAAAGIIGG 25
                                                                                                                                                                                            GTTCAGCTTTTTTGTACAAAGTTGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/63,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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Patent No. 6270969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25; Conservative
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STRANDEDNESS: bot
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Best Local Similarity
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US-09-233-492-15
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US-09-005-476-15
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APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Hemple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Choning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: NECOMBINATION SECONDINATION STATES
CURRENT APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1999-04-22
EARLIER FILING DATE: 1998-10-23
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEC ID NO 43
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Description of Unknown Organism: recombination
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
TUTLE OF INVENTION: Recombination Sites
TUMBER OF SEQUENCE: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
GTREET: 1100 New York Ave., N. W. Sulte 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 95.2%; Score 23.8; DB 3; Length 25; I. Similarity 88.0%; Pred. No. 0.24; 22; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.077;
has 0; Indels
                                                                                                                                                                                                   COMPURY: USA

ZIP: 2005-3934

ZIP: 2005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-UNN-1996
CIASSIFICATION INFORMATION:
TELEPHONE: 202-371-260
TELEPHONE: 202-371-260
TELEPHONE: 202-371-260
TELEPHONE: 202-371-260
SEQUENCE CHARACTERISTICS:
ENGTH: 25 base pairs
"VDF. nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GITCAGCITITITGIACAAGITGG 25
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Best Local Similarity
Matches 22; Conserv
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , MOLECULE TYPE:
PCT-US96-10082A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 7
US-09-296-280-43
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                                                                                                                                                                                                                                                                  APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPENDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: Machington
CITY: Wachington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
100.0%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.077;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
"TLING DATE: (Herewith)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Life Technologies, Inc.
8717 Grovemont Circle
Gaithersburg, MD 20884-9980
United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GTTCAGCTTTTTGTACAAGTTGG 25
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APPLICANT: Life Technologies, Inc. APPLICANT: Gaithersburg, MD 20884-95 APPLICANT: Gaithersburg, MD 20884-95 APPLICANT: United States of America
                                25
                                                              GITCAGCTTTTTTGTACAAAGTTGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: (Herewith)
CLASSIFICATION
PRIOR PELLICATION DATA:
PRIOR DATE: 12-JAN-1998
CLASSIFICATION TOWBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/63,002
FILING DATE: 07-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION:
                                                                                                                                                                        US-09-498-074-15; Sequence 15, Application US/09498074; Patent No. 6534264; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic aci
STRANDEDNESS: bot
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PCT-US96-10082A-15
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APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites

TITLE OF INVENTION: Recombination Sites

TORRESPONDENCE 35

CORRESPONDENCE ADDRESS:

ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600

CITY: Washington

STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23.4; DB 3; Length 25;
Pred. No. 0.34;
0; Mismatches 1; Indels
                                                                                     GOLDSTEIN & FOX, P.L.L.C
N. W. Suite 600
                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1999
CLASSIFICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIF: 2005-3934

ZIR: 2005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IRM PC compatible
OCHEVIER: PROCOMMENTE
SOFTWARE: Patentin Release #1.0, Version #1.30
                  HILE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTTCAGCTTTTTGTACAAGTTGG 25
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                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OMPUTER: READABLE PC COMPATIONS SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 10
18-09-005-476-11
Sequence 11, Application US/09005476
Patent No. 6171861
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, G(
STEET: 1100 New York Ave., N.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: both
MOLECULE TYPE: cDNA
US-09-233-493-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DP
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Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
                                                                                                                                                                                                    Sequence 11, Application US/09233493
; Sequence 11, Application US/09233493
; GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
ITILE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY. Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 93.6%; Score 23.4; DB 3; Length 25; Best Local Similarity 96.0%; Pred. No. 0.34; Matches 24; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTTCAGCTTTCTTGTACAAAGTTGG 25
                                              GITCAGCITITITIGIACAAAGIIGG 25
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELECOMONICATION:
TELECHONONICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: both
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US-09-233-493-16
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US-09-233-493-11
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STATE:
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RESULT 12
US-09-233-492-11
Sequence 11, Application US/09233492
Sequence 11, Application US/09233492
Patent No. 6270869
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: FLOPPY GISK
COMPUTER: FLOPPY GISK
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAM: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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                              Gricaecrircireracias deride 25
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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nes 24; Conserv
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Sequence 16, Application US/09005476
Patent No. 6171861
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 93.6%; Score 23.4; DB 3; Length 25; 96.0%; Pred. No. 0.34; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                    Query Match 93.6%; Score 23.4; DB 3; Length 25; Best Local Similarity 96.0%; Pred. No. 0.34; Matches 24; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION UNMERR: US/09/005,476
FILING DATE: herewith
CLASSIFFICATION:
PRIOR APPLICATION UNMER: 08/63,002
FILING DATE: 07-UN-1996
TELECHON NUMBER: 08/63,002
TELEPHONE: 202-371-260
TELEPHONE: 202-371-260
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANBENBES: both
TOPPLONE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                     25
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 GITCAGCITITITIGIACAAAGIIGG
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TELEPRINE: 202-3/1-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
'TONGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity
Matches 24; Conserva
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0; Mismatches
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                              RESULT 15
US-08-498-074-11
Sequence 11, Application US/09498074
; Patent No. 6534264
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ilarity 96.0%;
Conservative
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    24; Conservative
                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 3E
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KE
STREET: 1100 New Yorl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               nucleic acid
EDNESS: both
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Best Local Similarity
Matches 24; Conserv
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                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-498-074-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Was
STATE: DO
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
       Matches
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Sequence 16, Application US/09296280

Sequence 16, Application US/09296280

Sequence No. 6277608

September No. 6277608

APPLICANT: Brasch, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Fox, Donna K.

TILLE OF INVENTION: Recombination Sites

TILLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.2860007

CURRENT APPLICATION NUMBER: US/09/296,280

CURRENT PILING DATE: 1999-04-22

EARLIER FILING DATE: 1999-10-23

EARLIER FILING DATE: 1999-10-23

EARLIER FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LAND TABLES APPLICATION VARIABLES

MANDER OF SEQ ID NOS: 60

SEQ ID NO 16

LAND TABLES APPLICATION VARIABLES

LAND TABLES APPLICATION VARIABLES

MANDER OF SEQ ID NOS: 60

SEQ ID NO 16
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Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 93.6%; Score 23.4; DB 3; Length 25; Best Local Similarity 96.0%; Pred. No. 0.34; Matches 24; Conservative 0; Mismatches 1; Indels
                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Datentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 0-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STAPE: LODING: CDNA
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96.0%;
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Best Local Similarity
                Washington
                                                        COUNTRY: USA
ZIP: 20005-3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
US-09-296-280-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-233-492-16
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                                                                                                                                                                                                                                                                         APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 23.4; DB 4; Length 25; Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       SSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. 1100 New York Ave., N. W. Suite 600 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: PC-UGS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION NUMBER: 09/005,476
FILING APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELEFENON: 202-371-2600
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                                               1 GIICAGCITICITGIACAAAGIIGG 25
1 GTICAGCTITITIGIACAAAGTIGG 25
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US-09-498-074-16
Sequence 16, Application US/09498074
Sequence No. 6534264
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
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Gaps
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GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & POX, P.L.L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 93.6%; Score 23.4; DB 5; Length 25; Best Local Similarity 96.0%; Pred. No. 0.34; Matches 24; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: PCT/US96/10082A FILING DATE: 07-JUN-1996
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                              APPLICATION NUMBER: PCT/US96/10082A FILING DATE: 07-JUN-1996 CIASSIFFICATION: TELECATION: TELEPHONE: 202-371-2600 FILEFRAX: 202-371-2600 FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS: LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GITCAGCITITITGIACAAAGIIGG 25
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COMPUTER READMBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compacible
OPERATING SYSTEM: PC-DOS/MS-DOS
SUSTEMARE: Patentin Relace
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
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Best Local Similarity 96.0
Matches 24; Conservative
                                            SOFTWARE: Patentin ReleCURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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STATE: DC
COUNTRY:
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APPLICANT: 8717 Grovemont Circle
APPLICANT: 8717 Grovemont Circle
APPLICANT: 8717 Grovemont Circle
APPLICANT: Withersburg, MD 20884-9980
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
  TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS: ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23.4; DB 4; Length 25; Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
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                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-3934
COMBUTER READBALE FORM:
MEDIUM TYPE: FlOppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECUMNUM: 202-1/2 TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
TWATH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.6%;
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 25 base pa
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MOLECULE TYPE: CDNA
US-09-498-074-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 24; Conserv
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PCT-US96-10082A-11
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FILING DATE: herewith CLASSIFICATION:
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APPLICATION NUMBER: (
FILING DATE: 07-JUN-1
  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-005-476-9
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Matches
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                                                                 RESULT 19
US-09-233-493-9
is Sequence 9, Application US/09233493
j Patent No. 6143557
j Patent No. 6143557
j GENERAL INFORMATION:
j APPLICANT: Hartley, James L.
j TITLE OF INVENTION: Recombinational Cloning Using Engineered
j TITLE OF INVENTION: Recombination Sites
i CORRESPONDENCE ADDRESS:
j CORRESPONDENCE ADDRESS:
j ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
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Patent No. 6171861
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered LITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 89.6%; Score 22.4; DB 3; Length 25; Best Local Similarity 95.8%; Pred. No. 0.88; Matches 23; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPALIDLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
GTTCAGCTTTTTTGTACAAAGTTG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION: DATA:
RAPPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEPHONE: 202-371-2600
TELEPRAX: 202-371-2640
INFORMATION FOR SEC ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-005-476-9
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Gaps
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APPLICANT: Bratcley, James L.
APPLICANT: Bratcley, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SECURNCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: DC
COUNTRY: USA
ZIF: 20002-3934
COMPUTER RELABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: IEM PC compatible
COMPUTER: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
                                                                                       COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington STATE: DC COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 22.4; DB Pred. No. 0.88; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-JAN-1999
1:0-JAN-1999
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APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UMBER: 08/486,139
07-JUN-1995
                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMUNICATION INFORMATION:
TELECHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-233-492-9
; Sequence 9, Application US/09233492
; Patent No. 6270969
                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHRACTERISTICS: LENGTH: 25 base pairs TYPE: nucleic acid
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ilarity 95.8%;
Conservative
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us-10-055-001a-10.rni

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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; MOLECULE TYPE: CDNA
US-09-498-074-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
The 23; Conserva
      Washington
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                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 24
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APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTHER INFORMATION: Description of Unknown Organism: recombination; CTHER INFORMATION: products
US-09-296-280-9
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APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE 35
ADDRESSEE: STENDERSS.
ADDRESSEE: STENDERSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 22.4; DB 3; Length 25; Pred. No. 0.88; 1; Indels 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                   Query Match 89.6%; Score 22.4; DB 3; Length 25; Best Local Similarity 95.8%; Pred. No. 0.88; Matches 23; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER FILING DATE: 1998-10-24
NUMBER: OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                    24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 9, Application US/09296280 Patent No. 6277608
TELECOMMUICATION:
TELECOMMUICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYRE: nucleic acid
STRANDEDMESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Best Local Similarity
                                                                                                                                                                                                        ; MOLECULE TYPE: CDNA
US-09-233-492-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-296-280-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
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Gaps
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GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: Bit Technologies, Inc.
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: United States of America
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSIER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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COUNTRY: USA
ZIP: 20003-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ELBM PC Compatible
OPERATING SYSTEM: PC-0008/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Tarewith)
PRIOR APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION: NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 20-371-2540
INFORMATION FOR SED ID NO: 9: SEQUENCE CHARACTERISTICS:
LEMBTH: 25 base pairs
WYDE: number: acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: .....
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FTT:NG DATE: 07-UUN-1996
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Suite 600, 1919 Pennsylvania Ave., NW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM :
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
RIOR APPLICATION DATA:
APPLICATION NUMBER: 08/021,667
FILING DATE: 24-FEB-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 18, Application US/08410544; Patent No. 5607646; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 92.0
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                         Washington
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                                                                 USA
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US-08-410-544-18
                     CITY: Wa
STATE: D
COUNTRY:
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Sequence 42, Application US/09296280

Setent No. 6277688

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Temple, Gary F.

APPLICANT: Fox, Donna K.

TITLE OF INVENTION: Recombination Sites

FILE REPRENCE: 0942.286007

CURRENT APPLICATION NUMBER: US/09/296,280

CURRENT APPLICATION NUMBER: US 09/177,387

EARLIER APPLICATION NUMBER: US 09/177,387

SARLIER APPLICATION NUMBER: US 60/065,930

BARLIER FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PATENTING VET: 2.0

SEQ ID NO 42

LEARLIER FILING DATE: 2.20

SEQ ID NO 42
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US-08-021-667A-18
Sequence 18, Application US/08021667A
Sequence 18, Application US/08021667A
Sequence 18, Application US/08021667A
GENERAL INFORMATION:
APPLICANT: Value APPLICANT: Value APPLICANT: APPLICANT: POLYNUCLEOTIDE CAPTURING TIP AND TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli, Terry, Stout & Kraus
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
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88.0%; Score 22; DB 3; Length 25;
Best Local Similarity 79.2%; Pred. No. 1.3;
Matches 19; Conservative 5; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                       1; Indels
                                                                                                                                                                                                                                                                                     89.6%; Score 22.4; DB 5;
95.8%; Pred. No. 0.88;
trive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTTCAGCTTTTTGTACAAGTTG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                              1 Gircagcritirigiacaacric 24
                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                     23; Conservative
                                                                                                                                                                                                                           CDNA
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                     both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                   TOPOLOGY: bo
                                                                                                                                                                                                                                                  PCT-US96-10082A-9
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US-09-296-280-42
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APPLICANT: Okano, Kazunori
APPLICANT: Kambara, Hideki
TITLE OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: POLYNUCLEOTIDE PREPARATIVE METHOD AND DETECTION
TITLE OF INVENTION: METHOD USING SAME
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Attonelli, Terry, Stout & Kraus
STREET: Suite 600, 1919 Pensylvania Ave., NW
STATE: DC
COUNTRY: USA
ZIP: 20006
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
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ZIF: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/021,667A
FILING DATE: 19930224
CLASSIFOATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: TEATY, David T.
REGISTRATION NUMBER: 520.31930X00
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELECHMONICATION INFORMATION:
TELEFAX: 202-828-0380
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CURRENT APPLICATION DATA:
- APPLICATION NUMBER: US/08/410,544
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DNA (genomic)
YES
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WILMINTON STATE: DELAWARE
                              ; HYPOTHETICAL: Y
; ANTI-SENSE: NO
US-08-728-785A-18
   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 3
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Sequence 18, Application US/08728785A
Fatent No. 5817506
GENERAL INFORMATION:
APPLICANT: Okano, Kazunori
APPLICANT: Okano, Kanbara, Hideki
APPLICANT: OF INVENTION: POLYNUCLEOTIDE CAPTURING TIP AND
TITLE OF INVENTION: METHOD USING SAME
TITLE OF INVENTION: METHOD USING SAME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Antonelli, Terry, Stout & Kraus
STREET: Suite 1800, 1300 No. 5817506th Seventeenth St.
CITY: Arlington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
TINNO DATE:
CLASSIFICATION DATA:
FILINO DATE:
APPLICATION DATA:
FILING DATE:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
NAME:
TELEPHONE:
TELEP
                       REGISTATION NUMBER: 20,178
REGISTATION NUMBER: 520,178
RETERENCE/DOCKET NUMBER: 520,31930X00
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-828-0300
TELER: 248545
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE GIRARACTERISTICS:
LENGTH: 201 base pairs
TYPE: mucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTTCAGCTTTTTGTACAAGTTGG 25
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic);
HYPOTHETICAL: YES;
ANTI-SENSE: NO
US-08-410-544-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 703-312-6666
INFORMATION FOR SEQ ID NO: 1/
SEQUENCE CHARACTERISTICS:
LENGTH: 201 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
   Terry, David T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Antonelli
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Best Local Similarity
Matches 23; Conserv
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Score 21.8; DB 1; Length 201; Pred. No. 1.7;
                                                 2; Indels
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                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: FAHNESTOCK, STEPHEN F.
TITLE OF INVENTION: NOVEL RECOMBINANTLY PRODUCED
TITLE OF INVENTION: SPIDER SILK ANALOGS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: E. I. DU PONT DE NEMOURS AND COMPANY
STREET: 1007 MARKET STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD FOR WINDOWS 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/556,978B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                               0; Mismatches
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                                                                                              1 GTTCAGCTTTTTGTACAAGTTGG 25
                                                                                                                                         40 GricaGCriririnaracraaGrigg 64
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,600
FILING DATE: JUNE 15, 1993
ATTORNEY/ABENT INFORMATION:
NAME: FLOYD, LINDA AXAMETHY
REGISTRATION NUMBER: 33,692
REPERBENCE/DOCKET NUMBER: CR-9389-
TELECOMMUNICATION INFORMATION:
TELECHONE: 302-892-8112
                                                                                                                                                                                                             RESULT 29
US-08-256-978B-78/c
Sequence 78, Application US/08556978B
Patent No. 6268169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 30
US-07-590-988A-1
; Sequence 1, Application US/07590988A
; Patent No. 5227288
; Patent No. 5227288
; APPLICANT: Blattner, Frederick R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic) US-08-556-978B-78
    Query Match
Best Local Similarity 92.0%;
Matches 23; Conservative
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US-09-005-476-10

Sequence 10, Application US/09005476

GENERAL INFORMATION: Recombination Sites

INTIE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: SECONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600

COUNTRY: Washington YEASE.

STATE: DC COUNTRY: USA

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

OMPUTER: DATE: POPPY disk

COMPUTER: DATE: POPPY disk

COMPUTER: DATE: POPPY disk

COMPUTER: DATE: POPPY disk

SOFTWARE: PATICATION DATA:

APPLICATION NUMBER: US/09/005,476

FILING DATE: HORWITH NUMBER: US/09/005,476

FILING DATE: OT-UUN-1996

TELECOMMUNICATION DATA:

APPLICATION NUMBER: 202-371-2500

TELECOMMUNICATION SOC SEO IT NO. 10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 3; Length 25;
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          CLASSIFICATION
PRIOR APPLICATION
PRIOR APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1996
CLASSIFICATION:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEPHONE: 202-371-2600
TELEPRAX: 202-371-2640
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 22; Conserv
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US-09-233-493-10
is Sequence 10, Application US/09233493
is Patent No. 6143557
is GENERAL INFORMATION:
is APPLICANT: Hartley, James L.
is APPLICANT: Brasch, Michael A.
is TITLE OF INVENTION: Recombination Sites
in NUMBER OF SEQUENCES: 35
is CORRESPONDENCE ADDRESS:
is ADDRESSEE: STERRE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       87.2%; Score 21.8; DB 1; Length 7652; 92.0%; Pred, No. 2;
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COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette - 3.50 inch, 800Kb storage COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh OPERATING SYSTEM: Macintosh OPERATING SYSTEM: Macrosoft word 4.0 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/590,988A FILING DATE: 19901001

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Nicholas J. Seay

REGISTRATION NUMBER: 27,386

REFERENCE/DOCKET NUMBER: 3629691682

TELECOMMUNICATION INFORMATION:

TELEPRONE: (608) 251-9166

INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:

LENGTH: 7652 base pairs

TYPE: NUCLEIC ACID

STRANDENNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
       DNA Sequencing Vector with
Reversible Insert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: Other nucleic acid; DESCRIPTION: synthetic recombinant plasmid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTTCAGCTTTTTTGTACAAGTTGG 25
                                                         ...ukeSSEE: Quarles and Brady STREET: P.O BOX 2113 STREET: P.O BOX 2113 STREET: PRST WISCONSIN PLAZA CITY: WADISON COUNTY: U.S.A ZIP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 92.0
Matches 23; Conservative
TITLE OF INVENTION: DNA TITLE OF INVENTION: Reve NUMBER OF SEQUENCES: 1 CORRESPONDENCE ADDRESSEE: Quarles and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  circular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ANTI-SENSE: no
US-07-590-988A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL:
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TYPE: DNA ORGANISM: Unknown FEATURE:
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 36
US-09-498-074-10
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US-09-296-280-11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
ITILE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20.8; DB 3; Length 25; Pred. No. 4;
                                                           83.2%; Score 20.8; DB 3; Length 25; 91.7%; Pred. No. 4;
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STATE: DC

COUNTRY: USA

ZIF: 20005-3934

COUNTRY: USA

COUNTRY: USA

COUNTRY: USA

COMPUTER: TEMPAGE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DS

SOFTWARE: PARTICATION DATA:
APPLICATION NUMBER: US/09/233,492

FILING DATE: 20-JAN-1999

CLASSIFICATION NUMBER: 08/663,002

FILING DATE: 07-JUN-1996

CLASSIFICATION DATA:
APPLICATION NUMBER: 08/486,139

FILING DATE: 07-JUN-1995

CLASSIFICATION:
TELECOMMUNICATION: INFORMATION:
TELECOMMUNICATION: TELECOMMUNICATION:
TELECOMMUNICATION: DATA:
STELEBHONE: 202-371-2600

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
TUNFORMATION: DATA: DAT
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91.7%; Pred. No. 4,
0; Mismatches
                                                                                                                              0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 10, Application US/09233492
Patent No. 6270969
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                              22; Conservative
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 22; Conser
                                                                                         Best Local Similarity
Matches 22; Conserv
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US-09-296-280-10
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                                                                                                                                                                                                                                                                                                                                                     RESULT 33
US-09-233-492-10
US-09-005-476-10
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                                                               Query Match
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Sequence 11, Application US/09296280

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Donna K.

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.2850007

CURRENT APPLICATION NUMBER: US/09/296,280

CURRENT FILING DATE: 1999-04-22

EARLIER PLING DATE: 1999-10-23

EARLIER PLING DATE: 1999-10-24

NUMBER OF SEQ ID NOWER: US/097-10-24

NUMBER OF SEQ ID NOS: 60

SEQ ID NO 11

IENGTH: 25
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APPLICANT: Fox, Dorna K.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.285007
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT APPLICATION NUMBER: US/09/17,387
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1999-04-2.
EARLIER FILING DATE: 1999-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARER PATENTION VOICE: 2.0
SEQ ID NO 10
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTHER INFORMATION: Description of Unknown Organism: recombination of OTHER INFORMATION: products
US-09-296-280-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) OTHER INFORMATION: Description of Unknown Organism: recombination ; OTHER INFORMATION: products US-09-296-280-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
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Best Local Similarity 91.7%; Pred. No. 4;
Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20.8;
Pred. No. 4;
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Best Local Similarity 91.7%;
Matches 22; Conservative
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US-09-233-493-5
Sequence 5, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michaell A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 5; Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: Datent BM PC compatible
OPERATION SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
TELESTICATION:
TELESTRICATION:
TELEPHONE: 202-371-2600
TELEPRA: 202-371-2600
TELEPRA: 202-371-2540
INFORMATION POR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
"WIPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Washington
STATE: DG
COMPTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: BM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentl Nelease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION NUMBER: 09/005,476
FILING DATE: 07-JAN-1998
CLASSIFICATION STEER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GITCAGCITITIGIACAAAGIIG 24
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TELEBERONE: 202-371-260
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 91.77
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PCT-US96-10082A-10
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APPLICANT: 8717 Grovemont Circle
APPLICANT: 8717 Grovemont Circle
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
TITLE OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
                                                   APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPENDED ADDRESS:
ADDRESSEE: STERNE, KESSIER, GOLDSTEIN & FOX, P.L.L.C
STREET: Mashington
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83.2%; Score 20.8; DB 4; Length 25; ilarity 91.7%; Pred. No. 4; Conservative 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                     STATE: DC
COUNTRY: USA
ZID: 20005-3934

COMPUTER TEADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 10, Application PC/TUS9610082A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GITCAGCTITITIGIACAAGTIG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/63,002
FILING DATE: 07-UNN-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-UNN-1995
CLASSIFICATION:
FILING DATE: 07-UNN-1995
CLASSIFICATION:
TELEPHONE: 202-371-2600
ITELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 10: SEQUENCE CANDERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE:
US-09-498-074-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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Patent No. 6143557

GENERAL INFORMATION:
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites NUMBER OF SEQUENCES: 35
CORRESPENDENCE ADDRESS:
ADDRESSED: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81.6%; Score 20.4; DB 3; Length 25; 95.5%; Pred. No. 5.8; tive 0; Mismatches 1; Indels
                                                                                                                                                                  81.6%; Score 20.4; DB.3; Length 25; 76.0%; Pred. No. 5.8; tive 4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: DC
COUNTRY: USA
ZIP: 20005-3934
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PATENT: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
                                                                                                                                                                                                                                                                                1 GTTCAGCTTTYKTRTACNAAGTSGB 25
                                                                                                                                                                                                                                                      1 GITCAGCITITIGIACAAAGIIGG 25
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20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRICOR ADPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/683,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION
PRIOR APPLICATION
TILING DATE: 07-JUN-1996
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 12240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 95.5
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 25 base pairs
                                                                                                                                                                                                               19; Conservative
    SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
                                                                                        ; TOPOLOGY: both
; MOLECULE TYPE: CDNA
US-09-233-493-5
                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2
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US-09-233-493-12
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Gaps
RESULT 40
US-09-233-493-14
i Sequence 14, Application US/09233493
i Sequence 14, Application US/09233493
i Patent No. 6143557
i GENERAL INFORMATION:
i APPLICANT: Hartley, James L.
i TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
i TITLE OF SEQUENCES:
i CORRESPONDENCE ADDRESS:
i CORRESPONDENCE ADDRESS:
i STREET: 1100 New York Ave., N. W. Suite 600
i STREET: 100 New York Ave., N. W. Suite 600
i STREET: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
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                                                                                                                                                                                                                                                                                                                                                                                      ZIDS 2934

ZIDS 2005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
COMPUTER: PEN PC-DOS/MS-DOS
SOFTWARE: PATENTIN FC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7, 2003, 00:22:53
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APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CAGCTTTTTGTACAAAGTTGG 25
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APPLICATION NUMBER: 08/486,135
FILING DATE: 07-0UN-1995
CLASSIFICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search completed: November Job time: 29 secs
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Sequence

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US-09-233-493-11
                                         RESULT 1
pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                            ; Search time 28 Seconds (without alignments) 394.092 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 11,
Sequence 16,
                                                                                                                                                                                                                                                                                                                                                                                                 Description
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
         GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-233-493-16
US-09-005-476-11
US-09-005-476-11
US-09-233-492-11
US-09-233-492-11
US-09-296-280-16
US-09-498-074-11
PCT-US96-10082A-16
US-09-296-280-43
US-09-296-280-43
US-09-296-280-43
US-09-296-280-15
US-09-296-280-15
US-09-233-492-15
US-09-233-492-15
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US-09-233-492-15
US-09-233-492-15
US-09-233-492-10
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US-09-233-493-10
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US-09-005-476-14
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                                                                                                                                                              569978 seqs, 220691566 residues
                                                                                                                   1 gttcagctttcttgtacaaagttgg 25
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                                                                                                                                                                                                                            Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                November 6, 2003, 22:12:53
                                             OM nucleic - nucleic search, using sw model
                                                                                                                                     IDENTITY NUC Gapoxt 1.0
                                                                                                                                                                                                                                                                Issued_Patents_NA:
                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                 US-10-055-001A-11
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Match Length
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                                                                                                                                      Scoring table:
                                                                                                                       Sequence:
                                                                                                                                                                  Searched:
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                                                                                                     Title:
Perfect :
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Sequence 9, At
Sequence 9, At
Sequence 5, At
Sequence 5, At
Sequence 5, At
                                                          Sequence 14,
Sequence 9, A
Sequence 9, A
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Sequence 11, Application US/09233493
Sequence 11, Application US/09233493
Sequence 11, Application US/09233493
Sequence 11, Application Edition US/09233493
Septiment Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: Secombination Sites
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                     Sequence 9
                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                  Sequence
                 Sequence
                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATENTIAN PC COMPATIBLE
SOFTWARE: PATENTIAN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNDER: US/09/233,493
APPLICATION UNDER: US/09/233,493
US-09-233-492-14
US-09-296-280-14
US-09-296-280-14
US-09-296-280-42
US-09-296-10082A-14
US-09-296-10082A-14
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APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION UNMBER:
PILING DATE: 12-JAN-1998
CLASSIFICATION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-233-493-11
        888.0
888.0
888.0
883.2
883.2
883.2
883.2
881.6
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881.6
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APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSES: STERNE, KESSIER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 25; DB 3; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 25; Conservative 0; Mismatches 0; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: Herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-005-476-16
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                                                                                                                                                                                                                              COUNTRY:
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STATE:
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Sequence 16, Application US/09233493
Sequence 16, Application US/09233493
Sequence 16, Application US/09233493
Sequence 16, Application US/09233493
Patent NO. 6143520.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 3; Length 25; 100.0%; Pred. No. 0.015; ive 0; Mismatches 0; Indels
       Query Match 100.0%; Score 25; DB 3; Length 25; Best Local Similarity 100.0%; Pred. No. 0.015; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
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APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UN-1996
CLASSIPCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-UN-1995
CLASSIFICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 202-371-250
TELEFAX: 202-371-250
INFORMATION POR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                    1 GTTCAGCTTTCTTGTACAAAGTTGG
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: both MOLECULE TYPE: cl
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Gaps
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; Sequence 16, Application US/09005476
; Sequence 16, Application US/09005476
; Patent No. 6171861
; APPLICANT: Hartley, James L. APPLICANT: Hartley, Secondinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
ITLE OF INVENTION: Recombination Sites
ITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
    ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
CITY: Washington
STATE: DC
COUNTRY: USA
INTERIOR TYPE: FIOPPY disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: HEM PC compatible
COMPUTER: HEM PC compatible
COMPUTER: PATENTIN PO-DOS/MS-DOS
SOFTWARE: PATENTIN PATE:
STILNG DATE: herewith
CURRENT APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
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CLASSIFCATION
PRIOR APPLICATION DATE:
APPLICATION NUMBER: 08/663,002
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RESULT 3
US-09-005-476-11
Sequence 11, Application US/09005476
Patent No. 6171861
GENERAL INFORMATION:

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APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
CORRESPONDENCE: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 3; Length 25; ilarity 100.0%; Pred. No. 0.015; Conservative 0; Mismatched
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STAIR: DOUG-1934

ZIP: 20005-1934

ZIP: 20005-1934

COUNTRY: READBABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COURTENING SOFTEM: RC-1058/MS-1059
CURSEIFICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 202-371-2600
TELEFRAM: 202-371-2600
TELEFRAM: 202-371-2600
TELEFRAM: 202-371-2600
TELEFRAM: 202-371-2600
TELEFRAM: 202-371-2600
TELEFRAM: SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LANGTH: 25 base pairs
LANGTH: 25 base pairs
LANGTH: 25 base pairs
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FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEFAX: 202-371-2540
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 25; Conserva
                                                                                                                                                                                                                                     CDNA
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                                                                                                                                                                                                                              MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: DC
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APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE REFERENCE: 0942.2850007
CURRENT APPLICATION UNDBER: US/09/296,280
CURRENT FILING DATE: 1999-04-22
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0
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                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 3;
illarity 100.0%; Pred. No. 0.015;
Conservative 0; Mismatches 0
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APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UNN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-UNN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-UNN-1995
TELEPHONE: 202-311-2600
TELEPHONE: 202-311-2600
INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS:
LENGTH: 25 Dase pairs
TYPE: nucleic acid is
TYPE: nucleic acid is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 16, Application US/09296280; Patent No. 6277608; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: both MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 25; Conserv
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US-09-296-280-16
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TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: CDNA
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Best Local Similarity
Matches 25; Conserv
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; OTHER INFORMATION: Description of Unknown Organism: recombination
;; OTHER INFORMATION: products
15.09-296-280-16
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Patent No. 6534264
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSED: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                             ch 100.0%; Score 25; DB 3; Length 25; Similarity 100.0%; Pred. No. 0.015; 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCUNTRY: USA
ZIF: 20005-3934
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CORPOTER: IBM PC compatible
CORPANS: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION UNFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRX: 202-31-2540
INFORMATION FOR EQ ID NO: 11:
SEQUENCE: CHARACTERISTICS:
INMCMH: 25 base pairs
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DAFE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
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TYPE: nucleic acid
STRANDEDNESS: both
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MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                          LENGTH: 25
TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: DC COUNTRY:
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US-09-498-074-11
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Best Local Smillarity 100.0%; Score 25, DB 4; score 25; DB 48 there as 25; Cornesvative 0; Mismatches 0; Indels 0; Gaps 0; Or 1 | Cornesvative 0; Mismatches 0; Indels 0; Gaps 0; Indels 0; Indels 0; Indels 0; Gaps 0; Indels 0; Indels
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Sequence 43, Application US/09296280 Patent No. 6277608
  TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                    TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22; Conservative
                                                                                                                                nucleic acid
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Matches 22; Conserv
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ORGANISM: Unknown
                                                                                                                                                                                              MOLECULE TYPE:
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US-09-233-493-15
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US-09-296-280-43
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GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: Brasch, Midhael A.
ITILE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
APPLICANT: Life Technologies, Inc.
APPLICANT: 8717 Grovemont Circle
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; DB 5; Length 25; 100.0%; Pred. No. 0.015; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
                                                                                                                                                                                                     ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

PILING DATE:

FILING DATE:

TELECOMMUNICATION:

TELECOMMUNICATION:

TELEFHONE: 202-371-2600

TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs
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WEDLUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ELD FC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTTCAGCTTTCTTGTACAAAGTTGG 25
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                                                                                                                                                                                                                                                                           STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
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PCT-US96-10082A-16
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APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

APPLICANT: Brasch, Michael A.

APPLICANT: Brasch, Michael A.

APPLICANT: Femple, Gary F.

ITILE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

ITILE OF INVENTION: Recombination Sites

ITILE OF INVENTION: Recombination Sites

ITILE OF INVENTION RECOMBINATION SITES

GURRENT FILING DATE: 1999-10-23

BARLIER FILING DATE: 1999-10-23

BARLIER FILING DATE: 1999-10-23

BARLIER FILING DATE: 1999-10-24

NUMBER OF SEQ ID NOS: 60

SOFTHARE: PATENTIN VOICE: 20

SOFTHARE: PATENTIN VOICE: 20

SOFTHARE: PATENTIN VOICE: 20
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                                                         Gaps
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COTHER INFORMATION: Description of Unknown Organism: recombination of Unknown Organism: recombination US-09-296-280-43
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Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95.2%; Score 23.8; DB 3; Length 25; 88.0%; Pred. No. 0.051;
Query Match
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 25; Conservative 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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Gaps

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Sequence 15, Application US/09233492;
Sequence 15, Application US/09233492;
Patent No. 6270969
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
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Pred. No. 0.077;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                    Length 25;
                                                                                                                                                                                                                                                                                                    Query Match
93.6%; Score 23.4; DB 3; Length 2
Best Local Similarity 96.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GIICAGCITICITGIACAAAGIIGG 25
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UNN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-UNN-1995
CLASSIFICATION:
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION INFORMATION:
TELEPROMUNICATION 17-2000
TELEPROM: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                       1 GIICAGCIIICIIGIACAAAGIIGG
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFRMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 15: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93.6%;
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Best Local Similarity 96.03
Matches 24; Conservative
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TYPE: nucleic acid
STRANDEDNESS: both
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US-09-005-476-15
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US-09-233-492-15
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; Sequence 15, Application US/09005476
; Patent No. 6171861
; Patent No. 6171861
; APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
; APPLICANT: Brack, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
; TITLE OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSIER, GOLDSTEIN & FOX, P.L.L.C.
; STREET: Mashington
; CITT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005-3334

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493 FILING DATE: 20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTTCAGCTTTCTTGTACAAGTTGG 25
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herewith
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PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
                                            COUNTRY: USA
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPAN: 202-371-2600
TELEPAN: 202-371-2600
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: mucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-233-493-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 24; Conserv
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GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

TITLE OF INVENTION: Recombination Sites

TITLE OF INVENTION: Recombination Sites

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.2850007

CURRENT FILING DATE: 1999-10-23

EARLIER APPLICATION NUMBER: US 60/065,930

EARLIER FILING DATE: 1998-10-24

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 15

ILENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
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Patent No. 6534264

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
ITILE OF INVENTION: Recombinational Cloning Using Engineered
ITILE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSE: STERES, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.077;
Matches 24; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20005-3934
ZIP: 20005-3934
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
SUSRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FTT-NG DATE: (Herewith)
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APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
                                         Sequence 15, Application US/09296280 Patent No. 6277608
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Unknown
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US-09-498-074-15
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RESULT 16
US-09-296-280-15
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GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: White States of America
APPLICANT: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23.4; DB 5; Length 25; Pred. No. 0.077; 0; Mismatches 1; Indels
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Pred. No. 0.077;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                               1 GITCAGCITICITGIACAAAGITGG 25
                     PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION UNMERS: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEPACOMMUNICATION INFORMATION:
TELEPACOMMUNICATION TO TELEPACE: 202-371-2600
INFORMATION FOR ENG ID NO: 15: SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
"""DANDEDNESS: DOTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                      93.6%;
             FILING DATE: 07-JUN-1996
CLASSIFICATION:
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Best Local Similarity 96.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 96.04
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCT-US96-10082A-15
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Sequence 10, Application US/09005476

Patent No. 617181

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Harsch, Michael A.

TITLE OF INVENTION: Recombinational Cloning Using Engineered

TITLE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: 35
RESULT 19
US-09-233-493-10
US-09-233-493-10

Sequence 10, Application US/09233493

Patent No. 6143557

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.

TITLE OF INVENTION: Recombination Sites

IITLE OF INVENTION: Recombination Sites
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89.6%; Score 22.4; DB 3; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.22;
Matches 23; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Rioppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NOTE:

FILING DATE:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

CLASSIFICATION DATA:

APPLICATION NUMBER:

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

CLASSIFICATION NUMBER:

PRIOR APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

RELIGH DATE:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION NUMBER:

APPLICATION:

TELEPHONE:

TELEPHONE
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20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-233-493-10
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APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 3; Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: OF-ENWITH NOWER: 08/63,002
FILING DATE: 07-JUN-1996
TELECHMONICATION NUMBER: 08/63,002
FILING DATE: 07-JUN-1996
TELECHMONICATION INFORMATION:
TELEPAX: 202-371-2540
INFORMATION FOR EXQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
WATHER AS DATE OF THE OFFICE ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERALING SYSTEM: E-USON METALOR SOFTWARE: PATENTIN Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492 FILING DATE: 20-JAN-1999 CLASSIFICATION NUMBER: 08/663,002 PRIOR APPLICATION NUMBER: 08/663,002 FILING DATE: 07-JUN-1996 CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/466,139 FILING DATE: 07-JUN-1995 FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89.6%; Score 22.4; DB ilarity 95.8%; Pred. No. 0.22; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
CMDIUM TYPE: Floppy disk
CMDUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 10, Application US/09233492
; Patent No. 6270969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: both MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: DC
COUNTRY: USA
ZIP: 20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best_Local Similarity
Matches 23; Conserv
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Matches 23; Conserv
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                                                                                                                                                                           TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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US-09-296-280-10
i Sequence 10, Application US/09296280
i Sequence 10, Application US/09296280
i Patent No. 6277608
i GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: FOX. Donna K.
ITILE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850007
CURRENT APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1999-04-22
EARLIER FILING DATE: 1999-10-23
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SEQ ID NO 10
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 23
US-09-296-280-11
Sequence 11, Application US/09296280
Sequence 11, Application US/09296280
Patent No. 6277608
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Fox, Donna K.
TILE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TILE OF INVENTION: Recombination Sites
FILE REPERENCE: 0942.2850007
CURRENT APPLICATION NUMBER: US/09/296,280
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Pred. No. 0.22;
0; Mismatches 1; Indels
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Pred. No. 0.22;
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CLASSIFICATION:
TELECOMMUNICATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR EQG ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: nucleic acid
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Best Local Similarity 95.8%;
Matches 23; Conservative (
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1 Similarity 95.8%;
23; Conservative C
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MOLECULE TYPE: CDNA
US-09-233-492-10
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ORGANISM: Unknown
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Best Local S:
Matches 23
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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ABDIUM TYPE: Floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: DatentIn Release #1.0, Version #1.30

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/498,074

FILING DATE: (Herewith)

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,476

FILING DATE: 12-JAN-1998

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/663,002

FILING DATE: 07-JUN-1996

CLASSIFICATION:

PRIOR APPLICATION:

PRIOR 
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Pred. No. 0.22;
0; Mismatches 1;
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
BARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER APPLICATION NUMBER: US 60
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SORTWARE: 25
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
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95.8%;
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TYPE: nucleic acid
STRANDEDNESS: both
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us-10-055-001a-11.rni

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PRIOR APPLICATION DATA:
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Best Local Similarity
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Washington
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                                                                                             Gaps
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APPLICANT: 8717 Grovemont Circle
APPLICANT: 6717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-980
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSE: STRENE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Mashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 26
US-09-223-493-14
US-09-223-493-14
; Sequence 14, Application US/09233493
; Sequence 18, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Hartley, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCES. 35
; CORRESPONDENCE ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
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89.6%; Score 22.4; DB 5; Length 25;
Best Local Similarity 95.8%; Pred. No. 0.22;
Matches 23; Conservative 0; Mismatches 1; Indels
                                            Score 22.4; DB 4; Length 25;
Pred. No. 0.22;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STAIL.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYRE Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: APET PC COMPATIBLE
CONFURER: APET PC CONFORMS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
PTITING DATE: 07-UUN-1996
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS: LENGTH: 25 base pairs
                                                     89.6%;
                                                                                                  23; Conservative
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                                                     Query Match
Best Local Similarity
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              US-09-498-074-10
                                                                                                    Matches
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GENERAL STATICANT:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 25;
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APPLICATION NUMBER: US/09/005,476 FILING DATE: herewith
                                                                                                                                                         Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 3;
Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                               OPERATING SYSTEM: PC-LOS, MS-LOS
SOFTWARE: Patentin Release #1.0, Ver
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/23,493
FILING DATE: 20-JAN-1999
CLASSIFFICATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
PRICK APPLICATION DATA:
PRICK APPLICATION DATA:
PRICK APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRICK APPLICATION NUMBER: 08/466,139
FILING DATE: 07-JUN-1996
FILING DATE: 07-JUN-1996
FILING DATE: 07-JUN-1996
COUNTRY: USA
ZIP: 20005-3934
COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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; Sequence 14, Application US/09005476
; Patent No. 6171861
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100.0%; Pre
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CLASSIFICATION:
TELECOMMUNICATION:
TELEPHONE: 202-371-260
TELEFAX: 202-371-260
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
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ZIP: 20005-3934
COMPUTER READABLE FORM:
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Sequence 14, Application US/09296280

Sequence 14, Application US/09296280

Sequence 14, Application US/09296280

Setent No. 6277608

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Temple, Gary F.

APPLICANT: Peck, Donna K.

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.2850007

CURRENT PLING DATE: 1999-04-22

BARLIER PLING DATE: 1999-04-22

BARLIER PLING DATE: 1999-10-23

BARLIER PLING DATE: 1999-10-24

NUMBER OF SEQ ID NOWER: US 60/065,930

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 14

MANDEL SEC ID NO 14

MANDEL SEC ID NO 14

AND 14
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APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
ITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2860007
CURRENT APPLICATION NUMBER: US 09/177,387
BARLIER PILING DATE: 1998-10-23
BARLIER PILING DATE: 1998-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42
LENGTH: 25
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US-09-296-280-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: recombination
;; OTHER INFORMATION: products
US-09-296-280-14
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Pred. No. 0.33;
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88.0%; Score 22; DB
Best Local Similarity 100.0%; Pred. No. 0.3
Matches 22; Conservative 0; Mismatches
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                                        4 cagciricirgracaaagrigg 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Unknown
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US-09-296-280-42
                                                                                                                  RESULT 29
US-09-296-280-14
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APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: 35

CORRESPONDENCES: ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C

STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 88.0%; Score 22; DB 3; Length 25; Best Local Similarity 100.0%; Pred. No. 0.33; Matches 22; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                      Score 22; DB 3; Length 25;
Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONDITY: USA

CONFUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

COMFUTER: IBM PC compatible

COMFUTER: IBM PC compatible

COMFUTER: PC compatible

COMFUTER: PSTEM: PC-DOS/MS-DOS

SOFTWARE: PSTEM: Release #1.0, Version #1.30

SUSPENT APPLICATION DATA:

APPLICATION NUMBER: US/09/233,492

TIING DATE: 20-UAN-1999
                                                                                                                                                                                                                                                                                                                                         Query Match 88.0%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 0.3 Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-260
TELEPHONE: 202-371-260
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 CAGCTTTCTTGTACAAAGTTGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                         4 CAGCTTTCTTGTACAAAGTTGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
PELLOATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 14, Application US/09233492
Patent No. 6270969
APPLICATION NUMBER: 08/663,(FILING DATE: 07-JUN-1.996)
TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-2600
TELEPEAX: 202-371-2540
                                                                                                                    INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                              TOPOLOGY: both
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-233-492-14
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US-09-233-492-14
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Gaps

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Sequence 9, Application US/09233493
; Sequence 9, Application US/09233493
; Patent No. 6143557
; GENERAL INFORMATION:
    APPLICANT: Hartley, James L.
    APPLICANT: Brasch, Michael A.
    TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
    TITLE OF INVENTION: Recombination Sites
    TORRESPONDENCE ADDRESS:
    ADDRESSEE: STERNE, KESSIER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600
    CITY: Mashington
    STATE: DC
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
NUMBER OF EQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 5; Length 25;
Pred No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Indels
                                                                                                                                                   ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: FIDPPY disk
COMPUTER: IBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION UMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match

Best Local Similarity 100.0%; Pred. No. 0.3

Matches 22; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 both
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US-09-498-074-14
US-09-498-074-14
Sequence 14, Application US/09498074
Patent No. 6534264
SENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Braach, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                88.0%; Score 22; DB 4; Length 25; 100.0%; Pred. No. 0.33;
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                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.30
CUBRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DAIE: (Herewith)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Similarity 100.0%; Pred. No. 0.3 22; Conservative 0; Mismatches
                    Pred. No. 0.33
5; Mismatches
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PCT-US96-10082A-14
; Sequence 14, Application PC/TUS9610082A
; GENERAL INFORMATION:
; APPLICANT: Life Technologies, Inc.
; APPLICANT: 8717 Grovemont Circle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRICE APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION CANABLE CATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
                                                                                   1 GITCAGCTITCTIGIACAAGIIG 24
                                                                                                          1 GTTCAGCTTTYTTRTACWAASTKG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIF: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LENGTH: 25 base pairs
                      79.2%;
                      Best Local Similarity 79.2
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: ()
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1 GITCAGCITICITGIACAAAGITG 24
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CLASSIFICATION: 20-JAN-1999

CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/663,002

FILING DATE: 07-UN-1996

CLASSIFICATION NUMBER: 08/486,139

FILING DATE: 07-UN-1995

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139

FILING DATE: 07-UN-1995

CLASSIFICATION:
TELEPHONE: 202-371-2600

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                  24
                                         1 GTTCAGCTTTTTGTACAACTTG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83.2%;
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Best Local Similarity 91.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA
                                                                                                                                                                                                                                                                                                                                                                             Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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US-09-296-280-9
                                                                                                                                                                                                                                                                                                                                                                         CITY: Wa
STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-233-492-9
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APPLICANT: Barach, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: Mashington
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20.8; DB 3; Length 25; Pred. No. 1.1; 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                           Query Match

83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 91.7%; Pred. No. 1.1;
Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

ZIP: 20005-3934

CZIP: 20005-3934

CZIP: TRADABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/005,476

FILING DATE: herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GITCAGCITITIGIACAACTIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTTCAGCTTTCTTGTACAAGTTG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
FILING DATE: 07-JUN-1996
TELECOMMUNICATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-260
                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-UDN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 25 DASE PAIRS
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application US/09005476; Patent No. 6171861; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 91.7
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE: CDNA US-09-233-493-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     both
                                                                                                                                                                                                                                                                                                                         TOPOLOGY: both
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; MOLECULE TYPE:
US-09-005-476-9
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US-09-005-476-9
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Patent No. 6277608

GRNERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: FEASCH, Michael A.
APPLICANT: FOXION: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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Sequence 9, Application US/09233492
; Sequence 9, Application US/09233492
; Sequence 9, Application US/09233492
; Patent No. 6270084
; Patent No. 6270084
; APPLICANT: Brasch, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; TITLE OF INVENTION: Recombination Sites
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
   ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20.8; DB 3; Length 25; Pred. No. 1.1; 0; Mismatches 2; Indels
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1 GTTCAGCTTTCTTGTACAAAGTTG 24
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                                                                                                                                                                                                                                                                    Sequence 9, Application PC/TUS9610082A GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMULATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPRX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1: 25 base pairs
nucleic acid
DEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: CDNA
  CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20005-3934
                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                   RESULT 38
PCT-US96-10082A-9
                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
      ;
US-09-498-074-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE:
                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 39
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                                                                                                                                                                                                                                     FEATURE: OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
                                                                                                                                                                                                                                                                                                                                                                         .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TILE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                  Length 25
                                                                                                                                                                                                                                                                                                                                                                         2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CIIY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OORRATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILLING DATE: (Herewith)
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                Score 20.8; DB 3;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9;
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRICR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/63,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ 1D NO: 9:
SEQUENCE CLARACTERISTICS:
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; Patent No. 6534264
                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 91.7%;
Matches 22; Conservative
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STRANDEDNESS: both
                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 37
US-09-498-074-9
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                                                                                                                                               Gaps
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APPLICANT: AFFECTANT: AFFECTANT: APPLICANT: APPLICANT: AFFECTANT: AFFECTANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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// Sequence 5, Application US/09233493
// Sequence 5, Application US/09233493
// SERIEAL INFORMATION:
// APPLICANT: Hartley, James L.
// APPLICANT: Harsch, Michael A.
// TITLE OF INVENTION: Recombinational Cloning Using Engineered
// TITLE OF INVENTION: Recombination Sites
// NUMBER OF SEQUENCES:
// SORRESPONDENCE ADDRESS:
// ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.2%; Score 20.8; DB 5; Length 25; Best Local Similarity 91.7%; Pred. No. 1.1; Matches 22; Conservative 0; Mismatches 2; Indels
83.2%; Score 20.8; DB 4; Length 25; ilarity 91.7%; Pred. No. 1.1; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
GOMPUTER: IBM PC compatible
OMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILLIG DATE: PCT/US96/10082A
FILLIG DATE: O'-JUN-1996
CLASSIFICATION:
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Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81.6%; Score 20.4; DB 3; Length 25; 76.0%; Pred. No. 1.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA

ZIP: 20005-3934

COMPUTER REDABLE FORM:
MEDTUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIDLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
                                                                                                            COMMITER: USA
ZIF: 20005-3934
COMPUTER: Ploppy disk
COMPUTER: IBM PC compatible
COMPUTER: IPM PC compatible
COMPUTER: IPM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
1100 New York Ave., N. W. Suite 600
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                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Relection CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/286,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/286,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/286,139
FILING SAFICATION NUMBER: 08/2010
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/286,139
FILING SAFICATION NUMBER: 08/287
FILING DATE: 02-371-2640
FILING SAFICATION NUMBER: 202-371-2650
FILING SAFICATION SAFICATION SECULL SAFICATION S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 76.0°
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: both MOLECULE TYPE: cDNA
                                         Washington
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US-09-233-493-13
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PRIOR APPLICATION NATA:

APPLICATION NUMBER: 09/005,476

FILING DATE: 12-JRN-1998

CLASSIPETATION NUMBER: 08/663,002

PRIOR APPLICATION NUMBER: 08/663,002

FILING DATE: 07-JUN-1996

CLASSIPETATION: 08/486,139

FILING DATE: 07-JUN-1996

CLASSIPETATION: 08/486,139

FILING DATE: 07-JUN-1996

TELEPHONE: 202-371-2600

FILING DATE: 07-JUN-1996

TELEPHONE: 202-371-2600

FILING DATE: 07-JUN-1996

FILING DATE: 07-
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TYPE: nucleic acid
STRANDEDNESS: both
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US-09-233-493-10
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 1
US-09-233-493-10
                                   Sequence 10, Appl Sequence 9, Appli Sequence 9, Appli Sequence 9, Appli Sequence 11, Appl Sequence 11, Appl Sequence 16, Appl Sequence 16,
                                                                                                                                 6, 2003, 22:12:53; Search time 28 Seconds (without alignments) 394.092 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents NA:*
1: /cgn2 6/ptodata1/ina/5A_COMB.seq:*
2: /cgn2 6/ptodata1/ina/6A_COMB.seq:*
3: /cgn2 6/ptodata1/ina/6A_COMB.seq:*
4: /cgn2 6/ptodata1/ina/6B_COMB.seq:*
5: /cgn2 6/ptodata1/ina/PCTUS COMB.seq:*
6: /cgn2 6/ptodata4/l/ina/pcTUS COMB.seq:*
                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-233-493-10
US-09-005-476-10
US-09-233-492-10
US-09-233-492-10
US-09-498-074-10
PCT-US96-10082A-10
US-09-233-492-9
US-09-236-280-9
US-09-296-280-9
US-09-296-280-9
US-09-296-280-9
US-09-296-280-9
US-09-233-493-11
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US-09-296-280-16
US-09-296-280-16
US-09-296-280-16
US-09-498-074-11
US-09-498-074-11
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US-09-005-476-8
US-09-233-492-8
                                                                                                                                                                                                                                                                                                                                                                                   of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                         569978 seqs, 220691566 residues
                                                                                                                                                                                                         US-10-055-001A-5
25
1 gttcagctttcttgtacaaacttgt 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                               - nucleic search, using sw model
                                                                                                                                                                                                                                                                                     IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Match Length DB
                                                                                                                                     November
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   222
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                                                                                                                                                                                                             Title: .
Perfect score:
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No.
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Sequence
Sequence
                    Sequence
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                                                                                                  Sequence
                                                                                                        Sequence
      Sequence
                                                    Sequence
                                                           Sequence
              Sequence
    PCT - US96 - 10082A-8

US-09-296-280-11

US-09-233-493-3

US-09-233-493-3

US-09-233-493-15

US-09-233-493-15

US-09-233-492-3

US-09-233-492-3

US-09-296-280-15

US-09-296-280-15

US-09-498-074-15

PCT - US96-10082A-3

PCT - US96-10082A-3

PCT - US96-10082A-15

US-09-498-074-15
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## ALIGNMENTS

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Sequence 10, Application US/09233493

| Sequence 10, Application US/09233493
| Patent No. 641357
| GENERAL INFORMATION:
| Patent No. 641357
| GENERAL INFORMATION:
| APPLICANT: Barach, Michael A. |
| TITLE OF INVENTION: Recombination Sites
| TOWERSPONDINGE ADDRESS: CONDESSEE: STERNE, KESSIER, GOLDSTEIN & FOX, P.L.L.C
| STREET: 1100 New YORK AVE., N. W. Suite 600
| CITY: Washington STREET: Floppy disk
| COMPUTER: LIMP FC Compatible OFFRATION OF ACCOUNTS: INVENTION DATA: |
| APPLICATION NUMBER: US/09/233,493
| CLASSIFICATION NUMBER: 09/005,476
| FILING DATE: 12-JAN-1999
| CLASSIFICATION NUMBER: 08/663,002
| FILING DATE: 07-JUN-1996
| FILING DATE: 07-JUN-1996
| CLASSIFICATION NUMBER: 08/466,139 |
| FILING DATE: 07-JUN-1996
| CLASSIFICATION NUMBER: 08/466,139 |
| FILING DATE: 07-JUN-1996
| TELEPHONE: 202-371-260 |
| TELEPHONE: CHARACHISTICS: DATA |
| TOPOLOGY: DOLD |
| WOUNTER: DATA |
| WOUNTER: DATA |
| TOPOLOGY: DOLD |
| WOUNTER: DATA |
| TOPOLOGY: DOLD |
| WOUNTER: DATA |
| WOUNTER: DAT
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Sequence 10, Application US/09296280

Sequence 10, Application US/09296280

Patent No. 6277608

GENERAL INFORMATION:

APPLICANT: Bartley, James L.

APPLICANT: Temple, Gary F.

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.2850007

CURRENT FILING DATE: 1999-04-22

EARLIER FILING DATE: 1999-04-22

EARLIER PLINGATION NUMBER: US 60/055,930

EARLIER FILING DATE: 1999-10-23

EARLIER FILING DATE: 1999-10-23

EARLIER FILING DATE: 1999-10-23

SOFTWARE: PALENTIN UNSER: US 60/055,930

SOFTWARE: PALENTIN UNSER: US 60/055,930

SEAULISH ON INVERTION NUMBER: US 60/055,930

EARLIER FILING DATE: 1999-10-24

SOFTWARE: PALENTIN UNSER: US 60/055,930

SEAULISH ON 100

SEQ ID NO 10

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 3; Length 25; 100.0%; Pred. No. 0.013; tive 0; Mismatches 0; Indels
                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: RELIABLE FORM:
MEDIUM TYPE: FILIDOPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPARE: FALENCE FOR SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-JAN-1999
FILING APPLICATION:
PRIOR APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
CLASSIFICATION:
APPLICATION:
CLASSIFICATION:
CLASSIFICAT
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEPCOMOUNICATION INFORMATION:
TELEPAX: 202-371-2600
TELEFAX: 202-371-2500
; INFORMATION FOR EEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
LENGTH: 25 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-233-492-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 4
US-09-296-280-10
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| Patent No. 6270699
| GENERAL INFORMATION:
| APPLICANT: Hartley, James L. APPLICANT: Brasch, Michael A. TITLE OF INVENTION: Recombination Sites | NUMBER OF SEQUENCES: 35 | CORRESPONDENCE ADDRESS: ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 | CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels
Score 25; DB 3; Length 25;
Pred. No. 0.013;
Wismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: DC
COUNTRY: USA
ZIP: 20005-3934

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/63,002
FILING DATE: 07-UNA-1996
FILING DATE: 07-UNA-1996
FILING DATE: 07-371-2600
TELEFAX: 202-371-260
TELEFAX: 202-371-260

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
**PNYTH: 25 base pairs
   Query Match 100.0%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 0.0 Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GITCAGCTITCTIGIACAAACTIGT 25
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; Patent No. 6171861
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-005-476-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 3
US-09-233-492-10
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1 Gricagcrircrigiacaaacrigi 25
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APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
Brasch, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: both
; MOLECULE TYPE: CDNA
PCT-US96-10082A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 both
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US-09-233-493-9
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0
                                                                                                                                                                                                                                                         APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0.013;
0.013;
0; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/498,074

FILING DATE: (Herewith)

CLASSIFCATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/005,476

FILING DATE: 12-JAN-1998

CLASSIFICATION NUMBER: 08/63,002

FILING DATE: 07-JUN-1996

CLASSIFICATION NUMBER: 08/63,002

FILING DATE: 07-JUN-1996

CLASSIFICATION NUMBER: 08/486,139

FILING DATE: 07-JUN-1996

CLASSIFICATION NUMBER: 08/486,139

FILING DATE: 07-JUN-1995

CLASSIFICATION:

PRIOR APPLICATION NUMBER: 08/486,139

FILING DATE: 07-JUN-1995

CLASSIFICATION:

TELEPHONE: 202-371-2600

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARRACTERISTICS:

LENGTH: 25 base pairs

LENGTH: 25 base pairs

LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application PC/TUS9610082A
GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIF: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release
                                                                           Gricadcrircriciacaaacricr 25
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Sequence 10, Application US/09498074
Patent No. 6534264
GENERAL INFORMATION:
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: both
MOLECULE TYPE: CDNA
US-09-498-074-10
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PCT-US96-10082A-10
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Gaps
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Sequence 9, Application US/09233493

Patent No. 6143557

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Brack, Michael A.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
AUDRESSES: STERNES: 35
CORRESPONDENCE ADDRESS:
ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: Z0005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: Haw PC Compatible
COMPUTER: Bar PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/233,493
FILING DATE: Z0-UAN-1999
CLASSTETCHTON.
APPLICANT Brasch, Michael A.

TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF ENGUENCES: 31
NUMBER OF ESQUENCES: 31
STREET: 1100 New YORK Ave., N. W. Suite 600
CITY: Washington STREEN: COUNTY: Washington STREET: 100 New YORK Ave., N. W. Suite 600
CITY: Washington STREET: POONDES: 334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: PLoppy disk
COMPUTER: PC-DOS/NS-DOS
SOFTWARE: PATENTON DATE: PC-DOS/NS-DOS
CURRENT APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: O7-UNN-1996
CLASSIFICATION INFORMATION:
TELEFAX: 202-371-2600
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nucleic acid
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                                                                                                                                                                                                                                                                                                                                                    USA
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US-09-296-280-9
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                                                                                             US-09-233-492-9
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APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael L.
TILLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3; Length 25;
                                                                                                                                                                                                                                                                                                                                  Score 23.4; DB 3; Length 25;
Pred. No. 0.065;
0; Mismatches 1; Indels
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PATEN: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
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       FILING DATE: 07-JUN-1996
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION INPORMATION:
TELEPRAX: 202-371-2600
INFORMATION FOR SEQ ID No: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-005-476-9; Sequence 9, Application US/09005476; Patent No. 6171861
                                                                                                                                                                                                                                                                                                                                        93.6%;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                        LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 base pairs
                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 96.0
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nucleic acid
EDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 24; Conserva
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Sequence 9, Application US/09296280

Patent No. 6277608

Patent No. 6277608

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Transle, Gary F.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.285007

CURRENT APPLICATION UNDERS: US/09/296,280

CURRENT FILING DATE: 1999-04-22
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S-09-233-92-9
Sequence 9, Application US/09233492
Patent No. 6270969
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STRRET: 1100 New YORK AVE., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match

93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.065;
Matches 24; Conservative 0; Mismatches 1; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: PROPA DISK
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GITCAGCITICITGIACAAACITGI 25
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APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
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1 GITCAGCITICITGIACRACTIGI

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Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      both
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                                                                                                                                                                                                                                      PCT-US96-10082A-9
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                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
CORRESPONDENCE: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                          Query Match
93.6%; Score 23.4; DB 3; Length 25;
Best Local Similarity 96.0%; Pred. No. 0.065;
Matches 24; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CUBRENT APPLICATION DATA:
FILLING DATE: (Herewith)
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER PELLING NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
LENGTHARE: Patentin Ver. 2.0
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
ZIE: 20005-3934
COMPUTER READABLE PORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFTCATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILLING DATE: 07-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09498074
Patent No. 6534264
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUIENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 base pairs
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            both
                                                                                                                                                                                  TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
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APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: POWENTION: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
FILE REPERENCE: 0942.2850007
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1999-64-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                            Gaps
                                                                                                                                                                                                   APPLICANT: Life Technologies, Inc.
APPLICANT: Tife Technologies, Inc.
APPLICANT: 817 Carovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: United States of America
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23.4; DB 5; Length 25; Pred. No. 0.065;
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                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
F: 1100 New York Ave., N. W. Suite 600
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patentin Release #1.0, Version #1.30
SOPTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/100007
FILING DATE: 07-JIN.
    DB 4;
Score 23.4; DB
Pred. No. 0.065;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                            0; Mismatches
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                                                                                          25
                                                                                                                               1 Gricagcrirrirgiacaaacirgi 25
                                                                                                                                                                                                                                          Sequence 9, Application PC/TUS9610082A
GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: 8717 Grovement Circle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 13
US-09-296-280-42
; Sequence 42, Application US/09296280
; Betent No. 6277608
; GENERAL INFORMATION:
                                                                                            1 GITCAGCITICITGIACAACTIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative
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Query Match
Best Local Similarity 95.8%;
Matches 23; Conservative
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
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US-09-233-493-16
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CHER INFORMATION: Description of Unknown Organism: recombination
CHER INFORMATION: products
CHER INFORMATION: products
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Patent No. 6143557

GENERAL INPORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 22.6; DB 3; Length 25;
Pred. No. 0.15;
6; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER USA
ZIP: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IDM PC compatible
COMPUTER: IDM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIPICATION
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIPICATION
PRIOR APPLICATION NUMBER: 08/663,002
FILING DATE: 12-JAN-1996
CLASSIFICATION:
DELOS APPLICATION:
DELOS APPLICATIO
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN Vex. 2.0
SEQ ID NO 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTTCAGCTTTCTTGTACAAACTTGT 25
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APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 76.0%;
Matches 19; Conservative 6
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TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: both
MOLECULE TYPE: cDNA
US-09-233-493-11
                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-233-493-11
                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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Sequence In Propriet on US/09233493

Patent No. 6143557

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 25;
Score 22.4; DB 3; Length 25; Pred. No. 0.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
STATE: DC
CONTRY: USA
ZIP: 20005-3934
ZONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match

89.6%; Score 22.4; DB 3;
Best Local Similarity 95.8%; Pred. No. 0.18;
Matches 23; Conservative 0; Mismatches 1;
                                                    1;
                                                    0; Mismatches
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                                                                                                                                    1 GTTCAGCTTTCTTGTACAAAGTTG 24
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APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                  1 GITCAGCITICITGIACAACTIG 24
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; Patent No. 6171861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
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Gaps

; 0

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RESULT IS
RESULT IS
RESULT IN
RESULT IN
Sequence 11, Application US/09233492
Patent No. 6270593
GENERAL INFORMATION:
APPLICANT: Braich, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TOWNERS-SEE: STERNE, KESSIER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Mashington
STATE: DOCUMENT: RESULT OF AVE.
COUNTRY: USA
ZIP: 2006-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Patentin Release #1.0, Version #1.30
SOFTWARE: DATE: 20-JAN-1999
CLASSIFICATION DATE: 07-JUN-1995
TILING DATE: 07-JUN-1995
CLASSIFICATION DATE: 07-JUN-1995
TILING DATE: 07-JUN-1995
TILING DATE: 07-JUN-1995
TELERAX: 20-371-2600
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
TREEPX: 20-371-2600
INFORMATION CONSTRUCTS

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                                                                                                                                                                                                                                                                                                                                                                                                                   89.6%; Score 22.4; DB 3; Length 25; 95.8%; Pred. No. 0.18; tive 0; Mismatches 1; Indels
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APPLICATION NUMBER: 08/663,002
                                                                                                              INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 25 base pairs TYPE: mucleic acid STRANDEDNESS: both
                                  FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23; Conservative
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Best Local Similarity
Matches 23; Conserva
                                                                                                                                                                                                                                                                                                 TOPOLOGY: both

MOLECULE TYPE: CDNA

US-09-005-476-16
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 23; Conserv
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US-09-005-476-16
; Sequence 16, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.,
; APPLICANT: Harsch, Michael A.; TITLE OF INVENTION: Recombinational Cloning Using Engineered; TITLE OF INVENTION: Recombination Sites
                                        APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE DE INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSED: STERNE, SESSIER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STRTE: 100 No.
STRTE: 100 No.
STRTE: DOS
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMETIN NEW BATA:
APPLICATION NAMBER: US/09/005,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 89.6%; Score 22.4; DB 3; Length 25; Best Local Similarity 95.8%; Pred. No. 0.18; Matches 23; Conservative 0; Mismatches 1; Indels
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/005,476

FILING DATE: herewith

FILING DATE: herewith

PRIOR APPLICATION DATA:

PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: 08/663,002

FILING DATE: 07-JUN-1996

TELEFRACHION INFORMATION:

TELEFRAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs
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                                                                                                                                                                                                                                                                                                                                                                    ZIP: 20005-3934
COMPUTER READABLE FORM:
REDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       both
                      GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
STATE: DC
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
) OTHER INFORMATION: Description of Unknown Organism: recombination
) OTHER INFORMATION: products
US-09-296-280-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 89.6%; Score 22.4; DB 3; Length 25; Best Local Similarity 95.8%; Pred. No. 0.18; Matches 23; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
COUNTRY: USA
ZIP: 2005-3934
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: BM PC compatible
COMPUTER: IBM PC compatible
CORPTWARE: BATENTIN Release #1.0, Version #1.30
SUSPETMARE: Patentin Release #1.0, Version #1.30
; SOFTWARE: DATENTIN NUMBER: US/09/498,074
TT:NG DATE: (Herewith)
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN VET. 2.0
SOFTWARE: PATENTIN VET. 2.0
LENGTH: 25
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APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION:
TRILOG DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
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; Sequence 11, Application US/09498074
; Patent No. 6534264
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TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
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Patent No. 6277608

Patent No. 6277608

Patent No. 6277608

APPLICANT: Hartley, James L. APPLICANT: Brasch, Michael A. APPLICANT: Fox, Donna K. TILLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having FILE REFERENCE: 0942.2850007, CURRENT APPLICATION NUMBER: US/09/296,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                  | Sequence 16, Application US/09233492
| Patent No. 6270969
| GENERAL INPORMATION:
| APPLICANT: Hartley, James L. APPLICANT: Brasch, Michael A. TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites NUMBER OF SEQUENCES: 35 CORRESPONDENCE ADDRESS: ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 89.6%; Score 22.4; DB 3; Length 25; Best Local Similarity 95.8%; Pred. No. 0.18; Matches 23; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: DC
COUNTRY: USA
ZIP: 2006-3934
COMPUTER REABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION ONTA:
PRIOR APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION DAT
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                                   GTTCAGCTTTCTTGTACAAACTTG 24
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TELEFAX: 202-371-2540
INFORMATION FOR EQ. 1D NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25 base pairs
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STRANDEDNESS: both
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MOLECULE TYPE: CI
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                                                                                                                                                                                                           RESULT 19
US-09-233-492-16
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APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPENDENCE ADDRESSE: ATBLES STEER: S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 22.4; DB 4; Length 25; Pred. No. 0.18; 0; Mismatches 1; Indels
                                           Score 22.4; DB 4; Length 25;
Pred. No. 0.18;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDTUM TYBE: F.DOPPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATCHILIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE:
FILING DATE:
CLASSIFICATION:
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APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                   1 GITCAGCITICITGIACAAACIIG 24
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APPLICATION NUMBER: 08/486,139
ELLING DATE: 07-JUN-1995
CLASSIFICATION:
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Patent No. 6534264
GENERAL INFORMATION:
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TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
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                                                                  Query Match
Best Local Similarity 95.8%;
Matches 23; Conservative
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Best Local Similarity 95.8'
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ZIP: 20005-3934
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PCT-US96-10082A-11
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US-09-498-074-11
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; Sequence 11, Application PC/TUS9610082A

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APPLICANT: SITÉ "recentedigise, Inc.
APPLICANT: Barach, Michael A.
ITILE OF INVENTION: Recombinational Cloning Using Engineered
ITILE OF INVENTION: Recombinational Cloning Using Engineered
ITILE OF INVENTION: Recombination Sites
COUNTY: Variability Resombination Sites
ITILE OF INVENTION: Recombination Sites
COUNTY: Nathington STREENE SISSIER, COLDSTEIN & FOX, P.L.L.C
STREE: DC
SOUTHY: DC
SOUTH PROCESSION OF THE STREENE SISSIER, COLDSTEIN & FOX, P.L.L.C
STREE: DC
SOUTHY: DC
SOUTH SITES DC
SOUTH SEASON SITES DC
SOUTH SITES DC
SOU
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0

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Pred. No. 0.28;

100.08;

22; Conservative

Matches

Best Local Similarity

0; Mismatches

4 CAGCTTTCTTGTACAACTTGT 25

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Sequence 8, Application US/09233493
Sequence 8, Application US/09233493
PATEUR NO. 6143557
PAPLICANT: Hartley, James L.
APPLICANT: Harsch, Michael A.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & POX, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.6%; Score 22.4; DB 5; Length 25; 95.8%; Pred. No. 0.18; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPRES: USAS

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
APPLICATION NUMBER: 07-JUN-1995
CLASSIFICATION:
APPLICATION NUMBER: 07-JUN-1995
CLASSIFICATION:
APPLICATION NUMBER: 07-JUN-1995
CLASSIFICATION:
APPLICATION NUMBER: 07-JUN-1995
CLASSIFICATION:
APPLICATION:
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TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: both
MOLECULE TYPE: cDNA
PCT-US96-10082A-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1100 New CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: bo
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88.0%; Score 22; DB 3; Length 25;

Query Match

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APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                               APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Hartley, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSES: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88.0%; Score 22; DB 3; Length 25; 100.0%; Pred. No. 0.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 2005-3934
COMPUTER READBLE FORM:
MEDTION TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION

CLASSIFICATION

PRIOR APPLICATION DATA:

APPLICATION WUMBER: 08/663,002

FILING DATE: 07-UN-1996

TELEPHONE: 202-371-2600

TELEPHONE: 202-371-2540

INFORMATION FOR SEQ ID NO:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 CAGCITICITGIACAAACIIGI 25
CAGCTTTCTTGTACAACTTGT 25
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100.0%; Fre
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; Sequence 8, Application US/09233492
; Patent No. 6270969
                                                                                       US-09-005-476-8
; Sequence 8, Application US/09005476
; Patent No. 6171861
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 100.
Matches 22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: bo

MOLECULE TYPE:
US-09-005-476-8
                                                                                                                                                                                                                                                                                                                                                      STATE: DO
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us-10-055-001a-5.rni

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Gaps
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APPLICANT: Life Technologies, Inc.
APPLICANT: Saithersburg, MD 20884-9980
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 3.1
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                            Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                        88.0%; Score 22; DB 4;
100.0%; Pred. No. 0.28;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 8, Application PC/TUS9610082A GENERAL INFORMATION:
      CLASSIFICATION:
PRIOR APPLICATION
APPLICATION NUMBER: 08/486,139
PILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECHONE: 202-371-2600
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                25
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100.0%; Pre
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CLASSIFICATION:
TELECOMUNICATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
TOWGTH: 25 base pairs
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Best Local Similarity 100.0
Matches 22, Conservative
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 100.
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: both
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                   CDNA
                                                                                                                                                                                                                                                                              both
                                                                                                                                                                                                                                                                                ; TOPOLOGY: bo
; MOLECULE TYPE:
US-09-498-074-8
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Patent No. 6534264;
Patent No. 6534264;
GRERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Hartley, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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ZIP: Z0005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFCATION:
PRICK APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Rloppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: AttentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn Release #1.0, Version #1.30
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
TITING DATE: 20-UAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 88.0%; Score 22; DB Best Local Similarity 100.0%; Pred. No. 0.2 Matches 22; Conservative 0; Mismatches
                                                                                                                                                                                                      FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CAGCTTTCTTGTACAAACTTGT 25
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APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TOPOLOGY: both ; MOLECULE TYPE: cDNA US-09-233-492-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 both
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TOPOLOGY: bo
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                                                       US-09-233-493-3
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| Sequence 43. Application US/09296280
| Patent No. 6277608
| GENERAL INFORMATION:
| APPLICANT HARTIEY, James L.
| APPLICANT Emple, Gary F.
| APPLICANT Temple, Gary F.
| TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
| TITLE OF INVENTION: Recombination Sites
| TITLE OF INVENTION: Recombination Sites
| TITLE OF INVENTION NUMBER: US/09/296,280
| CURRENT FILING DATE: 1999-04-22
| CURRENT FILING DATE: 1999-04-23
| EARLIER FILING DATE: 1998-10-24
| NUMBER OF SEQ ID NOS: 60
| SEQ ID NO 43
| LENGTH: 25
                                                       GRUERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombination Sites
FILE REPERENCE: 0942.2850007
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT APPLICATION NUMBER: US 09/177,387
BARLIER FILING DATE: 1999-04-23
BARLIER FILING DATE: 1998-10-23
BARLIER FILING DATE: 1998-10-23
BARLIER FILING DATE: 1998-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 25
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US-09-296-280-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: Description of Unknown Organism: recombination ; OTHER INFORMATION: products US-09-296-280-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
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83.3%; Pred. No. 0.63;
cive 3; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 21.8; DB 3;
Pred. No. 0.34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GITCAGCITICITGIACAACTIGT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GTTCAGCTTTCTTGTACAAAGTGGT 25
US-09-296-280-11
; Sequence 11, Application US/09296280
; Patent No. 6277608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.2%;
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Best Local Similarity 83.3
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 92.03
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Unknown FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 31
US-09-296-280-43
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Gaps
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Sequence 3, Application US/09233493

Patent No. 6443557

GENERAL INFORMATION:
APPLICANT: Baratch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC.
STATE: DC.
STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 25;
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ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/23,493
FILING DATE: 20-JAN-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/663,002
FILING DATE: 07-JWN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JWN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JWN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JWN-1995
CLASSIFICATION:
RELEASSIFICATION:
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CLASSIFICATION:
RELEASSIFICATION:
RELEA
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80.0%; Pred. No. 0.96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTTCAGCTTTCKTRTACNAACTSGB 25
GTTCAGCTTTYTTRTACWAAGTTG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 80.03
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic aci
STRANDEDNESS: bot
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Gaps

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Patent No. 6171861

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STRRET: 1100 New York Ave., N. W. Suite 600
CITY: Nashington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 20.8; DB 3; Length 25; Pred. No. 0.96; 0; Mismatches 2; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: RIOPPY disk
MEDIUM TYPE: RIOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION: DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
FILING DATE: 07-JUN-1966
TELECOMMUNICATION INFORMATION:
TELECHONE: 202-371-5600
                                                                                                                                                                                                                                                                                                                                                                                                     DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
83.2%; Score 20.8; I
Best Local Similarity 80.0%; Pred. No. 0.96
Matches 20; Conservative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GITCAGCTITCTIGIACAACTIGT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GITCAGCTTTCTTGTACAAACTTG 24
             APPLICATION NOMBER: US/US/US/TROBING APPLICATION DATE: PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UN-1996
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-264
TELEPHONE: 202-371-264
TELEPHONE: 25 DASE PAIRS:
TYPE: NUCleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE YPE: CDNA
US-09-005-476-3
APPLICATION NUMBER: US/09/005,476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 91.7%;
Matches 22; Conservative
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US-09-005-476-15
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APPLICANT: Brasch, Michael A.
TITLE CANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 91.7%; Pred. No. 0.96;
Matches 22; Conservative 0; Mismatches 2; Indels
                              CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STEET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
                                                                                   CITY: Washing....
STAIE: DC
COUNTRY: USA
ZIP: 2006-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: BN PC compatible
COMPUTER: PREATING SYSTEM: PC-DOS/NS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
TITING DATE: 20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MN-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTTCAGCTTTCTTGTACAAACTTG 24
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APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
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Gaps

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US-09-296-280-3

'Sequence 3, Application US/09296280

'Patent No. 6277608

'Patent No. 6277608

'APPLICANT: Hartley, James L.

'APPLICANT: Brasch, Michael A.

'APPLICANT: Temple, Gary F.

'APPLICANT: Temple, Gary F.

'APPLICANT: Temple, Gary F.

'TITLE OF INVENTION: Recombination Sites

'TITLE OF INVENTION NUMBER: US 09/177,387

'EARLIER TILING DATE: 1999-04-22

'BARLIER FILING DATE: 1997-10-24

'NUMBER OF SEQ ID NOS: 60

'SOFTWARE: PatentIn Ver. 2.0

'SEQ ID NO 3

'LENGTH: 25
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NAME/KEY: OTHER
LOCATION: 18
OTHER INFORMATION: "n" may be any nucleotide
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
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COUNTRY: USA
ZIP: 20005-3934
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/233,492
FILLING DATE: 20-JAN-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 20.8; DB Pred. No. 0.96; 0; Mismatches
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APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 15:
LENGTH: 25 base pairs
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ilarity 91.7%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: CDNA US-09-233-492-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 22; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-296-280-3
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APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESSEE: STERNES, ESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                     APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Bngineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESSONDECE ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
83.2%; Score 20.8; DB 3; Length 25;
Best Local Similarity 80.0%; Pred. No. 0.96;
Matches 20; Conservative 3; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/233,492

FILING DATE: 0-JAN-1999

CLASSIFICATION DATA:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/63,002

FILING DATE: 07-JUN-1996

CLASSIFICATION:

PRIOR APPLICATION:

APPLICATION NUMBER: 08/486,139

FILING DATE: 07-JUN-1996

CLASSIFICATION:

TELECOMMUNICATION:

TELECOMMUNICATION:

TELECOMMUNICATION:

TELEFRHONE: 202-371-2600

TELEFRHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTTCAGCTTTCKTRTACNAACTSGB 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS_DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 37
US-09-233-492-15
Sequence 15, Application US/09233492;
Patent No. 6270969;
GENERAL INFORMATION:
                                                                                                                           Sequence 3, Application US/09233492; Patent No. 6270969; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: bot
; MOLECULE TYPE:
US-09-233-492-3
                                                                                 RESULT 36
US-09-233-492-3
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US-09-498-074-3
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                                                                                                                                                                                                                                            Sequence 15, Application US/09296280

Sequence 15, Application US/09296280

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Hartley, James L.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Fox, Donna K.

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.285007

CURRENT APPLICATION NUMBER: US 09/177,387

EARLIER APPLICATION NUMBER: US 60/065,930

EARLIER APPLICATION NUMBER: US 60/065,930

EARLIER APPLICATION NUMBER: US 60/065,930

EARLIER PLING DATE: 1999-10-24

NUMBER OF SEQ IN NOS: 60

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
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APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS: ADDRESSE: STERNE, KESSIER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 83.2%; Score 20.8; DB 3; Length 25; Best Local Similarity 91.7%; Pred. No. 0.96; Matches 22; Conservative 0; Mismatches 2; Indels
83.2%; Score 20.8; DB 3; Length 25; 80.0%; Pred. No. 0.96; ive 3; Mismatches 2; Indels
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ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

COMPUTER: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/498,074

FILING DATE: (Herewith)
                                                                                             1 GIICAGCIIICIIGIACAACIIGI 25
                                                                                                                                1 GTTCAGCTTTCKTRTACNAACTSGB 25
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Patent No. 6534264
GENERAL INFORMATION:
Query Match
Best Local Similarity 80.03
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Unknown
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
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/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-498-074-9
US-09-438-074-9
US-09-233-493-10
US-09-233-492-10
US-09-28-280-10
US-09-296-280-42
US-09-296-280-42
US-09-296-280-42
US-09-296-280-42
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US-09-296-280-42
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US-09-296-280-42
US-09-296-280-15
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US-09-296-280-16
                                                                                                                                                                                                                                   569978 seqs, 220691566 residues
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                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                       - nucleic search, using sw model
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Match Length
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Perfect score:
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28 20.8 83.2 25 4 US-09-498-074-11 Sequence 11, Appl 20 20.8 83.2 25 4 US-09-498-074-16 Sequence 16, Appl 31 20.8 83.2 25 5 PCT-US96-10082A-11 Sequence 16, Appl 32 20.4 81.6 25 3 US-09-233-493-8 Sequence 6, Appli 32 20.4 81.6 25 3 US-09-233-493-8 Sequence 8, Appli 35 20.4 81.6 25 3 US-09-05-476-8 Sequence 8, Appli 36 20.4 81.6 25 3 US-09-05-476-8 Sequence 8, Appli 36 20.4 81.6 25 3 US-09-05-476-8 Sequence 8, Appli 37 20.4 81.6 25 3 US-09-233-492-8 Sequence 8, Appli 38 20.4 81.6 25 3 US-09-233-492-8 Sequence 8, Appli 39 20.4 81.6 25 3 US-09-233-492-8 Sequence 8, Appli 41 20.4 81.6 25 3 US-09-233-492-8 Sequence 8, Appli 42 20.4 81.6 25 3 US-09-233-492-8 Sequence 8, Appli 42 20.4 81.6 25 3 US-09-233-492-8 Sequence 8, Appli 42 20.4 81.6 25 3 US-09-296-280-6 Sequence 6, Appli 20.4 81.6 25 3 US-09-296-280-6 Sequence 6, Appli 20.4 81.6 25 4 US-09-498-074-6 Sequence 6, Appli 20.4 81.6 25 4 US-09-498-074-8 Sequence 6, Appli 20.4 81.6 25 5 US-09-498-074-8 Sequence 6, Appli 20.4 81.6 25 5 US-09-498-074-8 Sequence 6, Appli 20.4 81.6 25 4 US-09-498-074-8 Sequence 6, Appli 20.4 81.6 25 4 US-09-498-074-8 Sequence 6, Appli 20.4 81.6 25 5 US-09-498-074-8 Sequence
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## AL IGNMENTS

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NESCONTY 1

Sequence 9, Application US/09233493

Sequence 9, Application US/09233493

Sequence 9, Application US/09233493

Sequence 9, Application US/09233493

PERCENTEL INFORMATION: Machael N. ApplicANT: Harlely Michael N. TITLE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDERS: 1300 New YORK AVE., N. W. SUITE 600

CITY: Washington New YORK AVE., N. W. SUITE 600

CITY: Washington New YORK AVE., N. W. SUITE 600

CITY: Washington OF COMPATION: RESPECT 1100 New YORK AVE., N. W. SUITE 600

CITY: Washington New YORK AVE., N. W. SUITE 600

CITY: Washington New YORK AVE., N. W. SUITE 600

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Sequence 9, Application US/09296280

Sequence 9, Application US/09296280

Setent No. 6277608

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

APPLICANT: Fox, Donna K.

APPLICANT: Fox, Donna K.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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US-09-296-280-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
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CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER FILING DATE: 1998-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTING DATE: 1997-10-24
SOFTWARE: PATENTING DATE: 1997-10-24
SOFTWARE: PATENTING DATE: 1997-10-24
SOFTWARE: PATENTING DATE: 1997-10-24
SOFTWARE: PATENTING DATE: 20
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                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07/JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07/JUN-1995
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , MOLECULE TYPE: CDNA US-09-233-492-9
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25, Conserv
                                               20005-3934
                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Unknown
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Best Local
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; Fatent No. 6270969
; GENERAL INFORMATION:
    APPLICANT: Hartley, James L.
    APPLICANT: Brasch, Michael A.
    TITLE OF INVENTION: Recombinational Cloning Using Engineered
    TITLE OF INVENTION: Recombination Sites
    NUMBER OF SEQUENCES: 35
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
    STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
Query Match 100.0%; Score 25; DB 3; Length 25; Best Local Similarity 100.0%; Pred. No. 0.075; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 25; DB 3; Length 25; 100.0%; Pred. No. 0.075; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/005,476

FILING DATE: herewith

CLASSIFTATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/663,002

FILING DATE: 07-JUN-1996

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEPHONE: 202-371-2540

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
                                                                                              1 GITCAGCITITIGIACAACTIGI 25
                                                                                                                                           Gricagcririririciacaacrici 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                           Sequence 9, Application US/09005476 Patent No. 6171861
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 1100
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Matches 25; Conserv
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US-09-005-476-9
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US-09-233-492-9
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FILING DATE: 20-UAN-1999
CLASSIFTCATION
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
FILING DATE: 12-JAN-1998
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLLGY: both
MOLECULE TYPE: cDNA
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                                                                                                                                                     STATE: DC COUNTRY:
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                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
IIILE OF INVENTION: Recombinational Cloning Using Bngineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
100.0%; Score 25; DB 4; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.075;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                  ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PILICATION NUMBER: US/09/498,074
FILIG DATE: (Herewith)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9, Application PC/TUS9610082A
GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
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                                          1 GTTCAGCTTTTTTGTACAAACTTGT 25
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APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIF: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                Sequence 9, Application US/09498074
Patent No. 6534264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 6
PCT-US96-10082A-9
                                                                                                      RESULT 5
US-09-498-074-9
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Gaps
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| Sequence 10, Application US/09233493
| Patent No. 6143557
| Patent No. 6143557
| Patent No. 614357
| APPLICANT: Hartley, James L.
| APPLICANT: Brasch, Michael A.
| TITLE OF INVENTION: Recombination Sites
| TITLE OF INVENTION: Recombination Sites
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: ADDRESSEE: CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
MUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSES: STERNE, KRSSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.0%; Score 25; DB 5; Length 25; Best Local Similarity 100.0%; Pred. No. 0.075; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC computer
COMPUTER: IBM PC computer
COMPUTER: IBM PC 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA

ZIP: 20005-3934

COMPUTER: ELDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPALIAL
COMPUTER: IBM FC COMPALIAL
COMPUTER: DEATH FC-DOS/MS-DOS
SOFTWARE: PATENTIN FC-DOS/MS-DOS
SOFTWARE: PATENTIN RELease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
CLASSIFICATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2540
TELEPHONE: 202-371-2540
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2600
SEQUENCE CHARACTERISTICS:
THEORYMATION FOR SEC ID NO: 9:
SEQUENCE CHARACTERISTICS:
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APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.6%; Score 23.4; DB 3; Length 25; 96.0%; Pred. No. 0.33; Live 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                  93.6%; Score 23.4; DB 3; Length 25; larity 96.0%; Pred. No. 0.33; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C. STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GirchGeirerigiacaaacirer 25
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FILING DATE.
CLASSIFICATION:
PRIOR APPLICATION NATA:
APPLICATION NUMBER: 08/486,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-005-476-10; Sequence 10, Application US/09005476; Patent No. 6171861
                                                              FILING DATE: 07-JUN-1995
CLASSIPICATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFRA: 202-371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 96.0
Matches 24; Conservative
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                                                                                                                                                                                : 25 base pairs
nucleic acid
EDNESS: both
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDNA
                                                                                                                                                                                                                                 ; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-493-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Washington
                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          both
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STRANDEDNESS:
                                                                                                                                                                                                                STRANDEDNESS:
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Best Local Simi
Matches 24;
                                                                                                                                                                                  LENGTH:
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Sequence 10, Application US/09296280
Fatent No. 6277608
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Fox, Donna K.
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850007;
CURRENT APPLICATION NUMBER: US/09/296,280
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Sequence 10. Application US/09233492

| Satent No. 6270969
| GENERAL INFORMATION:
| APPLICANT: Hartley, James L. APPLICANT: Hartley, James L. TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites NUMBER OF SEQUENCES: SECORRESPONDENCE ADDRESS:
| CORRESPONDENCE ADDRESS: ADDRESS: RESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600
| CITY: Washington CITY: Washington STATE: DC COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
WEDDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2500
TELEPAK: 202-371-2540
; INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 Dase pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILLING DATE: 07-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24; Conservative
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Matches 24; Conserva
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US-09-233-492-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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US-09-296-280-10
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CURRENT FILING DATE: 1999-04-22

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Gaps ÷

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TOPOLOGY: bo
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US-09-296-280-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 10, Application US/09498074

Patent No. 6534264
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STRRET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                    Query Match 93.6%; Score 23.4; DB 3; Length 25, Best Local Similarity 96.0%; Pred. No. 0.33; Matches 24; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OOMPUTER: IBM PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION:
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 Gricagcrircrigiacaaacricr 25
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2500
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                             TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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US-09-498-074-10
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US-09-296-280-42
Sequence 42, Application US/09296280
Patent No. 6277608
GENERAL INFORMATION:
APPLICANY: Hartley, James L.
APPLICANY: Temple, Gary F.
APPLICANY: Temple, Gary F.
APPLICANY: Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850007
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                                             Gaps
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                                                                                                                                                                                                                                 Sequence 10, Application PC/TUS9610082A
GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: Gaitherburg, MD 20884-9980
APPLICANT: Gaitherburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: Wisher, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
Query Match 93.6%; Score 23.4; DB 4; Length 25; Best Local Similarity 96.0%; Pred. No. 0.33; Matches 24; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & POX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: DC
COUNTRY: USA
ZIP: 20005-3934
ZIP: 20005-3934
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DCS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 23.4; DB 5;
Pred. No. 0.33;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/296,280 CURRENT FILING DATE: 1999-04-22
                                                                                         25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93.6%;
96.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 24; Conserv
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Best Local Similarity 95.8
Matches 23; Conservative
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                       Query Match
Best Local Similarity
Matches 23; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   both
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US-09-233-493-15
US-09-233-493-15
; Sequence 15, Application US/09233493
; Fatent No. 61435.7
; GENERAL INFORMATION:
APPLICANT: Harrley, James L.
APPLICANT: Harrley, Michael A.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered;
; TITLE OF INVENTION: Recombination Sites
; VUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                              Length 25;
                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OFFRATING SYSTEM: PC-DOS/MS-DOS
SOFFWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                         Query Match
90.4%; Score 22.6; DB 3;
Best Local Similarity 76.0%; Pred. No. 0.71;
Matches 19; Conservative 6; Mismatches 0;
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: US 60/065,930
EARLIER FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42
LENGTH: 25
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APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
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CLASSIFICATION:
PRIOR APPLICATION DATA:
FILING DATE: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 25 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: both
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                                                                                                                                                                 TYPE: DNA ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE:
US-09-233-493-15
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Sequence 15, Application US/09005476

Sequence 15, Application US/09005476

Sequence 17, Application

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

TITLE OF INVENTION: Recombinational Cloning Using Engineered

TITLE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESSE:

ADDRESSEE: STERNB, KESSIER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 New York Ave., N. W. Suite 600

CITY: Washington

CITY: Washington
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Sequence 15, Application US/09233492

Sequence 15, Application US/09233492

Patent No. 627098

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Harsch, Michael A.

TITLE OF INVENTION: Recombination Sites

TITLE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.

STREET: 1100 New York Ave., N. W. Suite 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               89.6%; Score 22.4; DB 3; Length 25; 95.8%; Pred. No. 0.86; 1; Indele Live 0; Mismatches 1; Indele
  DB 3; Length 25;
                                                     Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
199.6%; Score 22.4; DB ilarity 95.8%; Pred. No. 0.86; Conservative 0; Mismatches
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/63,002
FILING DATE: 07-JUN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 2005-3934
COMPUTER READABLE FORM:
WEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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Gaps ö

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GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89.6%; Score 22.4; DB 4; Length 25; 95.8%; Pred. No. 0.86;
          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION:
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       0; Mismatches
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GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: 8717 Grovemont Circle
APPLICANT: Gaithersburg, MD 20884-9980
                                                                                                       1 GITCAGCITITIGIACAAGIIG 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR ASPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UNN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139
FILING DATE: 07-UNN-1995
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GITCAGCTTTTTGTACAACTTG 24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIF: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Conservative
       23; Conservative
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MOLECULE TYPE: cl
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PCT-US96-10082A-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION NUMBER: US/09/296,280
CURRENT APPLICATION NUMBER: US/09/296,280
CURRENT FILING DATE: 1999-04-22
EARLIER APPLICATION NUMBER: US 09/177,387
EARLIER FILING DATE: 1999-10-23
EARLIER FILING DATE: 1999-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTING DATE: 100-24
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Pred. No. 0.86;
0; Mismatches 1; Indels
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                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
PEDFICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
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PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/63,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
IYPE: nucleic acid
STRANDENDNESS: both
                                                                  ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 15, Application US/09296280 Patent No. 6277608
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95.8%;
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Best Local Similarity 95.8%;
Matches 23; Conservative
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Best Local Similarity
Washington
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                                                   USA
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US-09-233-492-15
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SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
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  Conservative
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Best Local Similarity
Matches 22; Conserv
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    20;
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    Matches
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| Sequence 43, Application US/09296280
| Patent No. 6277608
| Patent No. 6277608
| General Information:
| APPLICANT: Hartley, James L. |
| APPLICANT: Temple, Gary F. |
| APPLICANT: Pemple, Gary F. |
| APPLICANT: Pown Recombination Sites |
| TITLE OF INVENTION: Recombination Sites |
| TITLE OF INVENTION: Recombination Sites |
| TITLE REFERENCE: 0942.285007 |
| CURRENT APPLICATION NUMBER: US 09/17,387 |
| EARLIER FILING DATE: 1999-04-22 |
| EARLIER FILING DATE: 1999-10-24 |
| WUMBER OF SEQ ID NOS: 60 |
| SOFTWARE: PatentIn Ver. 2.0 |
| SEQ ID NO 43 |
| LENGTH: 25 |
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APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 22.4; DB 5; Length 25;
Pred. No. 0.86;
0; Mismatches 1; Indels
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                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Ralease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
CLASSIFICATION:
TELECOMMUNICATION:
TELEFAHORE: 202-371-2600
TELEFAK: 202-371-2540
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 Gricagcritificaracaagrig 24
                                                                                                                                                                                                                            COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      89.6%;
95.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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COTHER INFORMATION:

US-09-296-280-43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT-US96-10082A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
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Gaps
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                                                                                                                                                                                                                                                APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE: 35
ADDRESSEB: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.2%; Score 20.8; DB 3; Length 25; 91.7%; Pred. No. 3.8;
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  Indels
                                                                                                                                                                                                                                                                                                                                                                        SEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.: 1100 New York Ave., N. W. Suite 600 Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER REDDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
  Mismatches
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APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UNN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMUNICATION:
TELEPHONE: 202-371-260
INFORMATION: 202-371-2540
INFORMATION: 202-371-2540
                                         1 GIICAGCIFFITIGIACAAACTIG 24
                                                                                 1 Gricagcirrrrrrracwaagrig 24
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Sequence 16, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
                                                                                                                                                                            Sequence 11, Application US/09233493
Patent No. 6143557
GENERAL INFORMATION:
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Gaps
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APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 83.2%; Score 20.8; DB 3; Length 25; Best Local Similarity 91.7%; Pred. No. 3.8; Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 20.8; DB 3; Length 25;
Pred. No. 3.8;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.: 1100 New York Ave., N. W. Suite 600
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 2005-3934
COMPUTER: ERDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
PatentIn Release #1.0, Version #1.30
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UN-1996
TELECOMUNICATION INFORMATION:
TELEFENCE: 202-371-2500
TELEFENCE: 202-371-2500
TELEFENCE: 202-371-2500
TELEFENCE: CAPACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTICAGCTITITIGIACAAACTIG 24
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/63,002
FILING DATE: 07-UN-1996
TELECOMMUNICATION INPORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 16, Application US/09005476 Patent No. 6171861 GENERAL INFORMATION:
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Best Local Similarity 91.7%;
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic act
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; MOLECULE TYPE:
US-09-005-476-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
STREET: 110
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US-09-005-476-16
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Patent No. 6171861

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Mashington
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: RECOMBINES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NAMBER: US/09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
                                                                                                                                                                                                                                            STAID.
COUNTY: USA
ZIP: 2005-1934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
....TTER: IBM PC COMPATIBLE
....TTER: TOW PC COMPATIBLE
....TTER: TOW PC COMPATIBLE
...TTER: TOW PC 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRICE APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
PRIOR APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/486,139
FILING APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDUIN TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMOTONICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 16: SEQUENCE CHARACTERISTICS: LENGTH: 25 base pairs TYPE: mucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-233-493-16
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US-09-005-476-11
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Sequence 16, Application US/09296280

Sequence 16, Application US/09296280

PAPELICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having

TITLE OF INVENTION: Recombination Sites

FILE REFERENCE: 0942.2860007

CURRENT APPLICATION NUMBER: US/09/296,280

CURRENT APPLICATION NUMBER: US 09/177,387

BARLIER APPLICATION NUMBER: US 60/065,930

EARLIER PILING DATE: 1999-10-24

NUMBER OP SEQ ID NOS: 60

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 83.2%; Score 20.8; DB 3; Length 25; Best Local Similarity 91.7%; Pred. No. 3.8; Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83.2%; Score 20.8; DB 3; Length 25;
                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SPECIALING SYSTEM: PC-DOS/MS-DOS
SPECIALICATION NUMBER: US/09/233,492
FLING DATE: 20-JAN-1999
CLASSIFICATION: DATA:
APPLICATION NUMBER: 08/663,002
FLING DATE: 07-UN-1996
CLASSIFICATION
PRIOR APPLICATION
FRICH APPLICATION:
CLASSIFICATION:
CLASSIFICA
1100 New York Ave., N. W. Suite 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
                                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-233-492-16
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                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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US-09-233-492-16

Sequence 16, Application US/09233492

Patent No. 6270969

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Brasch, Michael A.

TITLE OF INVENTION: Recombinational Cloning Using Engineered

TITLE OF INVENTION: Recombination Sites

WUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
ITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
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APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEPHONE: 202-371-2600
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                         1 dricadciricingracaaging 24
                                                                                                                                                                                                                                                                        ; Sequence 11, Application US/09233492; Patent No. 6270969
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TYPE: nucleic acid
STRANDEDNESS: both
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MOLECULE TYPE:
                                                                                                                                                                                                         RESULT 25
US-09-233-492-11
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Gaps

Matches

RESULT 28

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APPLICANT: Life Technologies, Inc.
APPLICANT: 8717 Growenon Circle
APPLICANT: Gaithersburg, MD 20884-9980
APPLICANT: United States of America
APPLICANT: United States of America
APPLICANT: TILLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 25;
                                                                                                                                                                                                              COMPRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,074
FILING DATE: (Herewith)
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELEFERX: 202-371-2600
TELEFERX: 202-371-2600
TELEFERX: 202-371-2540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.2%; Score 20.8; 1arity 91.7%; Pred. No. 3. Conservative 0; Mismatche
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Gricagerircrighacaaagrig 24
                                                                                                              SEE: STERNE, KESSLER,
: 1100 New York Ave.,
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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ZIP: 20005-3934
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K
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Matches 22; Conserv
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                                                                                                                                                                                                       USA
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                                                                                                                                                                                STATE: D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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US-00-498-074-11
Sequence 11, Application US/09498074
Patent No. 6534246
CENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83.2%; Score 20.8; DB 4; Length 25; 91.7%; Pred. No. 3.8;
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                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/498,074 FILING DATE: (Herewith)
                                2;
                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
           Pred. No. 3.8;
                                  Mismatches
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                                                                           1 GTTCAGCTTTTTTGTACAAACTTG 24
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APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
FILING DATE: 07-JUN-1995
CLASSIFICATION:
                                                                                                                     Grrchachrerichachadrig 24
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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US-09-498-074-16
; Sequence 16, Application US/09498074
; Patent No. 6534264
; PATENL INFORMATION:
; APPLICANT: Hartley, James L.
                                  ;
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
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           91.78;
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TYPE: nucleic acid
STRANDEDNESS: both
                                  22; Conservative
                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KI
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Matches 22; Conserv
           Best Local Similarity
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MOLECULE TYPE:
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Patent No. 6143557
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20.4; DB 3; Length 25; Pred. No. 5.6; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
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ZITE: DC
COUNTRY: USA
ZITE: DC
COUNTRY: USA
ZITE: DC
COMPUTER: ELADABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: ELADABLE FORM:
MEDIUM TYEE: Floppy disk
COMPUTER: DAY
COMP
                                                                     1 GITCAGCITITITIGIACAAACTIG 24
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Patent No. 6143557
GENBRAL INFORMATION:
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Best Local Similarity 95.5%;
Matches 21; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic ació
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US-09-233-493-6
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                                                                                                                                                                                                                          RESULT 32
US-09-233-493-6
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GENERAL INFORMATION:
APPLICANT: Life Technologies, Inc.
APPLICANT: Grichersburg, MD 2084-9980
APPLICANT: Grichersburg, MD 2084-9980
APPLICANT: United States of America
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 91.7%; Pred. No. 3.8;
Matches 22; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 25;
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-JUN-1996
CLASSIFTATION:
TELEPHONE: 202-371-260
TELEPHONE: 202-371-2540
TELEPHONE: 202-371-2540
TELEPHONE: 25 Dase pairs
SEQUENCE CHARACTERISTICS:
LENGTH: 25 Dase pairs
TYPE: nucleic acid
TYPE: nucleic acid
TYPE: DOTALDATED
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDLUM TYPE: FLOPDY disk
COMPUTER: IBM PC compatible
OCHENTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10082A
FILING DATE: 07-UWN-1996
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83.2%; Score 20.8; DB 5;
91.7%; Pred. No. 3.8;
tive 0; Mismatches 2;
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TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
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TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity
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PCT-US96-10082A-11
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PCT-US96-10082A-16
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APPLICATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
                     FILING DATE: 20-JAN-1999
CLASSIFICATION
PROR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 12-JAN-1998
CLASSIFICATION DATA:
APPLICATION DATA:
CLASSIFICATION:
BILING DATE: 07-JUN-1995
CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION:
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         22 CTGCTTTTTGTACAAACTTGT 1
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APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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STATE: D
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
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Patent No. 6143557

GENERAL INPORMATION:
APPLICANT: Brasch, Micheel A.
ITITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: Washington
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.6%; Score 20.4; DB 3; Length 25; 95.5%; Pred. No. 5.6; 1ive 0; Mismatches 1; Indels
                     CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PELLOATION NUMBER: US/09/233,493
FILING DATE: 20-JAN-1999
                                                                                                                                                                                                                                                                                                                          APPLICATION.
FILING DATE: 20-JAN-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION STAR.
PRIOR APPLICATION NUMBER: 08/63,002
FILING DATE: 07-JUN-1996
CLASSIFICATION: 07-JUN-1996
CLASSIFICATION: DATA: APPLICATION NUMBER: 08/63,139
FILING DATE: 07-JUN-1996
CLASSIFICATION: DATA: APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1996
CLASSIFICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: TELECOMMUNICATION: SEQUENCE CHARACTERISTICS: TENGTH: 25 DASE PAİRE
                                                                                                        STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
WEDIUM TYPE: FLOPDY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/WS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4 CAGCTTTTTTGTACAACTTGT 25
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Best Local Similarity 95.53
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-233-493-33/c
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Gaps
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US-09-05-476-6
Sequence 6, Application US/09005476
Fatent No. 6171861
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: STREET: 1100 New York Ave., N. W. Suite 600
CITY: Mashington
                                                        .
0
Query Match
81.6%; Score 20.4; DB 3; Length 25;
Best Local Similarity 95.5%; Pred. No. 5.6;
Matches 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDITUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: ELM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,476
FILING DATE: herewith
CLASSIFICATION:
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CURRENT APPLICATION DATA:

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION:
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION
PRIOR APPLICATION DATA:
PRILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/63,002
FILLING DATE: 07-UNN-1996
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEPHONE: 202-371-2540
TELEPHONE: 202-371-2540
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CAGCITITIGIACAACTIGI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 crecriririgiacaaacrist 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Sequence 6, Application US/09233492; Patent No. 6270969
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25 base pairs
  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
EDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) MOLECULE TYPE: CDNA
US-09-005-476-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 21; Conservi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         both
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US-09-005-476-8

J Sequence 8, Application US/09005476

Sequence 8, Application US/09005476

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSIER, GOLDSTEIN & FOX, P.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600

CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .
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Patent No. 6171861
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF ENGINEERICAL Recombination Sites
NUMBER OF SEQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81.6%; Score 20.4; DB 3; Length 25; 95.5%; Pred. No. 5.6;
                                                                                           81.6%; Score 20.4; DB 3; Length 25; 95.5%; Pred. No. 5.6; 1; Indels cive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/005,476

FILING DATE: herewith

CLASSIFICATION NUMBER: 08/663,002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/663,002

FILING APPLICATION INFORMATION:

TELEPHONE: 02-371-2600

TELEPHONE: 202-371-2600

TELEPHONE: 202-371-2540

INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs

TYPE: modific acid

STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 5.6;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: DC
COUNTRY: USA
ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4 CAGCTTTTTTGTACAAACTTGT 25
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Best Local Similarity 95.5
Matches 21; Conservative
                                                                                           Query Match
Best Local Similarity 95.5
Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CDNA
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-005-476-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: both
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US-09-005-476-33/c
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ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
WEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
PILING DATE: herewith
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Gaps ô DB 3; Length 25; 1; Indels

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GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Mashington STATE: DC COUNTRY: USA ZIP: 20005-3934 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 8, Application US/09233492; Patent No. 6270969; Patent No. 6270969; GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Hartley, James L., TITLE OF INVENTION: Recombinational Cloning Using Engineered; TITLE OF INVENTION: Recombination Sites NUMBER OF SEQUENCES: SECORESPONDENCE ADDRESS: CORRESPONDENCE ADDRESS: GORRESPONDENCE ADDRESS: GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
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                                                                                                                                                                                                                                                                                                                     Query Match 81.6%; Score 20.4; DB 3; Length 25; Best Local Similarity 95.5%; Pred. No. 5.6; Matches 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 81.6%; Score 20.4; DB 3; Length 25; Best Local Similarity 95.5%; Pred. No. 5.6; Matches 21; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA

ZIF: 20005-3934

COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE:
CLASSIFICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4 CTGCTTTTTTGTACAAACTTGT 25
CLASSIFICATION:
TELECOMMUNICATION INFORMATION:
TELEPHOR: 202-371-2540
TELEPAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: mucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 8:SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: both
; MOLECULE TYPE: cDNA
US-09-233-492-8
                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA
US-09-233-492-6
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Gaps
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             Sequence 33, Application US/09233492
Batent No. 6270969
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSED: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81.6%; Score 20.4; DB 3; Length 25; 95.5%; Pred. No. 5.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/233,492
FILING DATE: 20-JAN-1999
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UN-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-UN-1995
CLASSIFICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELEFAK: 202-371-260
TELEFAK: 202-371-250
TELEFAK: 202-371-254
INPORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
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Job time: 28 secs
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EDNESS: both
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Best Local Similarity
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US-09-233-492-33/c
                                                                                                                                                                                                                                                                                   STATE: D
COUNTRY:
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19-DEC-1996.
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Oligonuclectide #1
Recombination site
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Escherichia coli c
Escherichia coli c
                                                                                                                                                                                        2003, 21:05:38; Search time 111.5 Seconds (without alignments) 605.255 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:
| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:
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1: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*
2: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*
3: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1982.DAT:*
4: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
5: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1983.DAT:*
6: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
7: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1985.DAT:*
8: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
9: /SIDS1/gcgdata/geneseq/geneseqn-embl/NA1988.DAT:*
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|SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
|SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
|SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                             - nucleic search, using sw model
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AAD14444
AAF55745
AAF55750
AAC87876
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Maximum DB seq length: 200000000
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Match Length
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                               Copyright
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                                                                                                                             OM nucleic
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Lambda phage Int r Core sequence of r Core sequence of r Recombination site Recombination site Artificial plant c Artificial plant c Phage-lambda recom	site mocke ombination or plasmid or plasmid or plasmid or plasmid or plasmid ination pl	plasmid poo plasmid poo plasmid poo tor vector p tor vector p tor vector p core region nucleotide # core region nucleotide # tore region nucleotide # tore region richia coli	Core sequence of r Recombination site Artificial plant c Phage-lambda recom Att site nucleotid Recombination site Donor plasmid pDON
			4 ABQ81127 S ACC44664 S ABT16634 2 AAS06179 S ABZ58732 1 AACS5382
7 7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	223 2033 2004 4208 470 627 937	5156 5584 21 18691 18691 25 25 25 25 25 25 25 25 25 25 25 25 25	
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## ALIGNMENTS

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AAT48225 standard; DNA; 25 BP.

AAT48225;

AAT48225;

T 20-OCT-1997 (first entry)

E attp2,P3 core region.

Att recombination site; core region; mutation; enhance; recombination; vector; subcloning; regulation; exchange; ss.

Synthetic.

N W09640724-Al.

Synthetic.

A 07-JUN-1996; 96W0-US10082.

C 07-JUN-1995; 95US-0486139.

X LIFE-) LIFE TECHNOLOGIES INC.

Brasch MA, Hartley JL;

R WPI; 1997-065168/06.

N Nucleic acids, vectors and methods to obtain chimeric nucleic acid - using recombinant proteins and engineered recombination sites in
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                                            AAT48210-25 are att recombination site core region DNA sequences. The core region has at least one engineered mutation that enhances recombination in vitro in the formation of a Cointegrate or Product DNA. These core regions can be incorporated into novel vector donor DNA molecules. The nucleic acids, vectors and methods of the invention are used to obtain chimeric nucleic acid using recombination proteins and engineered recombination sites in vitro or in vivo. The improved specificity, speed and yields of the invention facilitates DNA or RNA subcloning, regulation or exchange useful for any related purpose, e.g. in vitro recombination of DNA segments, and in vitro or in vivo insertion or modification of transcribed, replicated, isolated or genomic DNA or modification of transcribed, replicated, isolated or genomic DNA or
                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NAMS) comprising: (a) combining in vitro or in vivo: (1) at least one insert donor molecules (IDMS) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMS) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or more sites which do not recombine with each other; and (3) one or more sites which do not recombination proteins; (b) incubating the combination to site specific recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the wethods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that
                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                    Score 25; DB 18; Length 25;
Pred. No. 0.11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cloning; donor; recombination site; vector; chimeric; ss.
                                                                                                                                                                                                                                                                              0; Indels
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                                                                                                                                                                                                                                       100.0%; Scc.
100.0%; Pred. No. v.
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                                                                                                                                                                                                                                                                                                                        1 GTTCAGCTTTCTTGTACAAAGTTGG
                         Claim 14; Page 56; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hartley JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 25; Conservative
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 or in vivo
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                                                                                                                                                                                                                                         Gaps
have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention.
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                                                                                                                                                                               Length 25;
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                                                                                                                 Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
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l for recombination cloning.
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95US-0486139.
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25; Conserv
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                                                                                                                                                                     Query Match
Best Local {
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Fri Nov

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/organism="Homo sapiens"
                                                                                                                                                                  1201 bp
                                                                                                                                                                                   AL544813 Homo sapiens PLACENTA
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/clone="CS0DI012YK20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                           31 CWGCTTTTTTGTACAACTTGW 10
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                                                                                                                                                                                                                                               AL544813.2 GI:31266654
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                                                                                                                                                                                                                                                                                         Homo sapiens (human)
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Matches 20; Conservative
                                                                                                                                                                                                                                                                                                          Homo sapiens
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BX355712/c
                                                                                                                                                                                   DEFINITION
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AUTHORS
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JOURNAL
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TITLE
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KEYWORDS
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KEYWORDS
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/mol_type="mRNA"

/db xref="taxon:966"

/clone="CSODEGOTYB08"

/tissue_type="PLACENTA"

/clone lib="Homo sapiens PLACENTA"

/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized." 36 others
                                                /organism="Homo sapiens"
/mol_type="mxnA"
/db_xref="taxon:9606"
/clone="CSODCOUZYEOS"
/clone="Ib="Homo sapiens NEUROBLASTOWA COT 25-NORMALIZED"
/clone="Ib="Homo sapiens NEUROBLASTOWA COT 25-NORMALIZED"
/clone="lat strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMYSPORT 6 vector. Library was normalized."

18 a 332 c 362 g 209 t 39 others
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AL541966 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE007YB08
AL541966
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BP 191 91006 EVRY cedex - France
BRMA11: Seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8896.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODE007DA04Qpl&cluster=8896.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODE007DA04Qpl.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                     84.8%; Score 21.2; DB 13; Length 1190; 90.9%; Pred. No. 5.5e+02; ive 2; Mismatches 0; Indels 0;
Faraday Avenue Genoscope sequence ID : CSODC002AC03QP1.
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Pred. No. 5.5e+02;
2; Mismatches 0; Indels 0
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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                Location/Qualifiers
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ilarity 90.9%;
Conservative
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Matches 20; Conserv
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AUTHORS
TITLE
JOURNAL
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KEYWORDS
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p mRNA linear EST 31-MAY-2003
COT 25-NORMALIZED Homo sapiens CDNA
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

240 c 255 g 315 t 67 others
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                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
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Li, W.B., Gruber,C., Jessee,J., and Polayes,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRail: sequefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was canterfucted by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 79.r For milliformation about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODIO12BFIONRPiccluster=79.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO12BFIONPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         On Feb 15, 2001 this sequence version replaced gi:12877293. Contact: Genoscope
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                                                                                                                                                                                                                                                                                                                                                                                  Li W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length CDNA libraries and normalization Unpublished
                                                             clone CSODI012YKZO 3-PRIME, mRNA sequence.
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Pred. No. 5.5e+02;
2; Mismatches 0
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Fri Nov

BASE COUNT ORIGIN

Matches

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DEFINITION

ACCESSION

VERSION KEYWORDS SOURCE

BX375648/c

RESULT 35

ORGANISM

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia; Butheria, Primates, Catarrhini; Hominidae, Homo.

E 16, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization

L Unpublished
On Feb 15, 2001 this sequence version replaced gi:12905303.

Contact: Genoscope Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: segref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
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Library was constructed by Life Technologies, a division of
Library was conscope.cns.fr/
cgi-bin/dluster.cgi?seq=CSODG001AA010Pl&cluster=3074.f. Contact :
Feng Liang Email : fliangelifetech.com URL :
Library Avenue Genoscope acquence ID : CSODG001AA010Pl.

Library Avenue Genoscope cauchom Library Compania Library Avenue Genoscope acquence ID : CSODG001AA010Pl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue type="B CELLS (RAMOS CELL LINE)"
/coll line="RAMOS CELL LINE"
/colne lib="Homo saptens B CELLS (RAMOS CELL LINE)"
/cone lib="Homo saptens B CELLS (RAMOS CELL LINE)"
/note="Wetcor: PCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and ECCRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY Cedex - France
BP 191 91006 EVRY Cedex - France
BP 191 91006 EVRY Cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9817.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
ggi-bin/cluster.cgi?seq=CSODC002AC03QP1&cluster=9817.f. Contact :
Feng Liang Email : fliang@lifecech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1190)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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/db_xref="taxon:9606"
/clone="CS0DG001YA01"
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Matches 20
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8X375648 Homo sapiens NEGROBIASTONA COT 25-NORMALIZED Homo sapiens
CDMA clone CSODC015YH12 5-PRIME, mRNA sequence.
BX375648
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/db_xref="taxon:9506"
/clone="CSODCOISYH12"
/tissue type="musuroBascoma COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/clone_list strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 221 c 268 g 272 t 18 others
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1 (bases 1 to 1067)
1 (Ja. M., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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AL559630 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: segref@genoscope.ons.fr, Web : www.genoscope.cns.fr
library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3245.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
ogi-bin/cluster.cgi?seq=CS0DC015DD06QPl&cluster=3245.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DC015DD06QPl.
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                                                                                      Length 995;
                                                                                  Score 21.2; DB 13;
Pred. No. 5.4e+02;
2; Mismatches 0;
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AL559630
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BP 191 91006 EVRY cedex - France
   188 t
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EST.
                                                                                         84.8%;
90.9%;
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Best Local Similarity
Matches 21; Conserv
                                                                                         Query Match
Best Local Similarity
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DEFINITION

ACCESSION

VERSION

KEYWORDS SOURCE

RESULT 36 AL559630/c

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BASE COUNT

ORIGIN

FEATURES

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Gaps

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/organism="Homo sapiens"

/mol_type="mRNA"

/mol_type="mRNA"

/db_tref="texan:9606"

/clone="CSODF077FD0"

/dev_stage="FETAL BRAIN"

/dev_stage="FETAL BRAIN"

/dov stage="fetal"

/dov and the strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

vector. Library was not normalized."

2 others
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/tissue type="NEUROBLASTOMA"
/clone lib="HGmc sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed
with a NotI-clied() primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr/
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3874.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSIDA002ZA08QPl&cluster=3874.r. Contact:
Feng Liang Bmail: filang@lifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSIDA002ZA08QPl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 995)
BX445504

BX445504 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone CSODA005YA10 5-PRIME, mRNA sequence.
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Pred. No. 5.4e+02;
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/db_xref="taxon:9606"
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95.5%;
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BX445504/c
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/db_xref="texon:9606"
/db_xref="texon:9606"
/dbe="CSODE006Y108"
/tissue type="plaCENTA"
/clone lib="Home sapiens PlaCENTA"
/clone lib="texon complete"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a Not1-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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AL538458 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CSODF027YP04 5-PRIME, mRNA sequence.
AL538458
                                                 DA#17226
BX417226 Homo sapiens PLACENTA Homo sapiens cDNA clone CSODE006YI08
5-PRIME, mRNA sequence.
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Genoscope - Centra cada - France
Bm 119 191006 EVNY cada - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fullength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODE006BE046PI.
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                                                                                                                                                                                                                                                  Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 1201)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 946)
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Contact: Genoscope Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5628.f For
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Matches 22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished
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AL538458/c
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                          RESULT 32
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EST 15-MAY-2003

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Gaps

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3 TCAGCTTTTTTTTGTACAACTTGT 25
                                                                                                                                                                                                                                                                                                                                                                                         39 TCTGCTTTTTGTACAAACTTGT 17
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Homo sapiens
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Best Local Similarity
Matches 22; Conserv
                                                                                                                                                                                                                                                                                                      Similarity
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Best Local
                                                                                                                                                                                                              BASE COUNT
ORIGIN
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ORGANISM
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue type="THYMUS"
/clone_lib="Homo sapiens THYMUS"
/clone_lib="Homo sapiens THYMUS"
/clone_lib="Homo sapiens THYMUS"
/note="Vector: pcWSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMVSPORT 6 vector.
Library was not normalized.
1 89 orhers
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BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4028.f For
more information about this cluster, see
http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSODCO18AC10QP1
&cluster=4028.f. Contact: Feng Liang Email: fliang@lifetech.com
VRL: http://tullength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODCO18AC10QP1.
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                                                                                                                                                                                                              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5630.r For
more information about this cluster, see
http://www.genoscope.ns.fr/
cgi-bin/cluster.cgi?seq=cS0CAP004DE06QP1&cluster=5630.r. Contact :
http://fulllength.invitrogen.com/InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0CAP004DE06QP1.
Location/Qualifiers
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BX332991 Homo sapiens NEUROBLASTOWA COT 25-NORMALIZED Homo sapiens CDNA clone CSODCO18YE19 5-PRIME, mRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1132)
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                  Li, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
                                                                                                                                                     Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP004YJ12"
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Best Local Similarity
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                                                                                                                            Unpublished
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BX332991/c
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ORGANISM
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JOURNAL
                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 622.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODIO75CD01QP1&cluster=622.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fullInength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODIO75CD01QP1.
Location/Qualifiers
rce 1..1201
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/mol type="minus" cre-compared by the first state of the prime and compared by the prime and com
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/clone_lib="PtwCENTA COT 25-NORWALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORWALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMNSPORT 6 vector. Library was normalized."
316 c 356 g 196 t 79 others
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1 (Dases 1 to 1201)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   85.6%; Score 21.4; DB 13; Length 1201; 95.7%; Pred. No. 4.6e+02; ive 0; Mismatches 1; Indels 0;
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/db_xref="taxon:9606"
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EX456900 Homo sapiens THYMUS Homo saplens cDNA clone CS0CAP004YJ12 S-PRIME, mRNA sequence.
EX456900
EX456900.1 GI:31019269
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/clone_lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; lst strand cDNA was primed with a NotI-olise(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector.
                                                                                                                                                                                                                                                                                                                                                1119 bp mRNA linear EST 15-MAY-2003 BX437057 Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP004YN12 5-PRHE, mRNA sequence.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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Genoscope - Centre National de Sequencage
BP 191 91006 EWRY cedex - France
BP 191 91006 EWRY cedex - France
BP 191 91006 EWRY cedex - France
BRail: Seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
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Library was constructed by Library Web :
Location/Qualifiers
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88.0%; Pred. No. 4.5e+02;
iive 1; Mismatches 2; Indels 0;
                                                                                 Length 1071;
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     others
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                                                                                 Score 21.4; DB 13;
Pred. No. 4.5e+02;
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338 c 256 g 206 t
                                                                                                                                    0; Mismatches
     314
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0CAP004YN12"
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  250
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BX437057.1 GI:30781537
                                                                                 Query Match
Best Local Similarity 95.7%;
Matches 22; Conservative
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Best Local Similarity
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     181
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BX456900/c
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SOURCE
ORGANISM
BASE COUNT
ORIGIN
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BX437057/c
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BP 191 91006 EVRY cedex - France
BMail: sequencescope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9540.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAKO18DEDINM1ccluster=9540.f. Contact :
Feng Liang Email: fliang@lifetech.com URL
http://fulllength.invitrogen.com/ InVitroden Corporation 1600
Faraday Avente Genoscope sequence ID : CSOBAKO18DEDINM1.
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                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/mol type="mRNA"
/mol type="mRNA"
/db xref="taxon:9606"
/clone="CS0DCOOSYBLS"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BcoR V
sites of the pCNVBPORT 6 vector. Library was normalized."
a 260 c 217 g 382 t 3 others
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BX329663 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens CDNA clone CSODCO23YN14 3-PRIME, mRNA sequence.
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR v
sites of the pCMVSPORT 6 vector. Library was normalized."
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 10184.r For
more information about this cluster, see
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAK013CF02NM1&cluster=10184.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://wlllength.invitrogen.com/ invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAK013CF02NM1.
Location/Qualifiers
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85.6%; Score 21.4; DB 13; Length 1035;
Best Local Similarity 95.7%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 1; Indels 0;
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/clone="CS0DC023XN14"
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BX329663.1 GI:30340861
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/tissue type="FFFAL LIVER"

/dev_stage="fetal"

/dev_stage="fetal"

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was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pcMVSPORT 6

vector. Library was not normalized."

vector. Library was 160 t 3 others
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cgi-bin/cluster.cgi?seq=CSOBAKO59DB03NM1&cluster=7650.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAKO59DB03NM1.
Location/Qualifiers
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pCMYSPORT 6 vector. Library was normalized."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 953)
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Similarity 88.0%; Pred. No. 4.5e
22; Conservative 0; Mismatches
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BX372606 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens CDNA clone CSODCO05YB15 3-PRIME, mRNA sequence.
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and ECOR V
sites of the pUNVSPORT 6 vector. Library was normalized."
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BX372532 Homo sapiens NEUROBLASTOMA COT 10-NORMALIZED Homo sapiens CDNA clone CSODB007YB13 3-PRIME, mRNA sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1035)
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1. (Dases 1 to 965)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization
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Contact: Genoscope

Bp 191 91006 EVRY codex - France

Bp 191 91006 EVRY codex - France

Bmail: seqret@genoscope.cns.fr, Web : www.genoscope.cns.fr

Library was constructed by Life Technologies, a division of

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Best Local Similarity 95.7%; Pred. No. 4.5e+02;
Matches 22; Conservative 0; Mismatches 1;
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Genoscope - Centre National de Sequencage
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/clone="CSODB007YB13"
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1550.r For
more information about this cluster, see
http://www.genoscope.cns.fr,
cgi-bin/cluster.cgi?seq=CSOBAKO52DH04NM1&cluster=1550.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAKO52DH04NM1.
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//clone_lib="Homos sapiens PLACENTA COT 25-NORMALIZED"
//note="list strand cDNA was primed with a Not1-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
signesred with Not I and cloned into the Not I and EcoR V
sites of the pCWNSPORT 6 vector. Library was normalized."
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cgi.bin/cluster.cgi?seq=cS0AM009DC11QP1&cluster=7793.f. Contact :
reps Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0AM009DC11QP1.
       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 891)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Genoscope - Centre National de Sequencage
BP 191 91006 BVRY cedex - France
Email: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7793.f Formore information about this cluster, see
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                                                                         1. W.B., Gruber, C., Jessee, J., and Polayes, D. Full-length cDNA libraries and normalization Unpublished
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Full-length cDNA libraries and normalization
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/db_xref="taxon:9606"
/clone="CS0DI015YF12"
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BX373155 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CS0DI015YF12 3-PRIMB, mRNA sequence.
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/dev_stage="fetal"
/dev_stage="fetal"
/dov_stage="fetal"
/dovestage="fetal"
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318 c 262 g 291 t 77 others
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Livitrogen. This sequence balongs to sequence cluster 9373.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODW008AE05QPi&cluster=9373.r. Contact :
Feng Liang Email : fliangellietech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODW008AE05QPI.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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/db_xref="taxon:9606"
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 95.r For more
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMYSPORT 6 vector. Library was normalized."
140 c 217 g 340 t 169 others
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
BX363509 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED
Homo sapiens cDNA clone CS0DL001YD08 5-PRIME, mRNA sequence.
BX363509
                                                                                                                                                                                                                                                      Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. Li Dases; 1 to 1201)
Li W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length, CDNA libraries and normalization
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BP 191 91006 EVRY cedex - France
Bmail: seqrefègenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Linvitrogen. This sequence belongs to sequence cluster 2356.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODL001DB040Plscluster=2356.r. Contact
Feng Liding Email: fliang@lifetch.com URL: Contact
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODL001DB04QPl.
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Pred. No. 3.8e+02;
1; Mismatches 0
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Similarity 95.5%;
21; Conservative
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primer. Five prime and enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSEORT 6 vector. Library was normalized."
32 a 290 c 326 g 241 t 112 others
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1088.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=SODNKO05CB06QP1&cluster=1058.f. Contact :
Feng Liang Email: fliang@lifetech.com URL:
http://fullhength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODKO05CB06QP1.

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digested with Not I and cloned into the Not I and BCOR V
sites of the pCMVSPORT 6 vector. Library was normalized."
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length, cDNA libraries and normalization
information about this cluster, see http://www.genoscope.cns.fr/cgi-bin/cluster.cgi?seq=CSIAI018ZE07QPI&cluster=95.r. Contact : Feng Liang Email : fliangelifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSIAI018ZE07QPI.
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sites of the pCWVSPORT 6 vector. Library was normalized."
3 244 c 116 others
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339 c 352 g 250 t 37 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5023.r For
http://www.genoscope.cns.fr/
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=cSoDIO81CCO6QP1&cluster=5023.r. Contact :
Feng Librag Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO81CCO6QP1.
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On Feb 15, 2001 this sequence version replaced gi:12894503
Contact: Genoscope
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Homo sapiens
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Best Local Similarity
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ALSS4071/c
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                         /Organizem= nown Septems
//mol_type="mRDNA"
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/clone="CSODP003YB02"
/tissue type="fetal"
/dev_stage="fetal"
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and EcoRV sites of the pCMVSPORT 6
vector. Library was not normalized."
56 a 295 c 337 g 237 t 73 others
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1077.f For
more information about this cluster, see
thttp://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI012AG06QP1&cluster=1077.f. Contact :
ferpg Liang Email : fliangedifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI012AG06QP1.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
                                                                    Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3257.f,
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSIAF001ZF02QF1.

Location/Qualifiers
1. 1198
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Contact: Genoscope Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - Prance
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ilarity 95.5%; Pred. No. 3.8e+02;
Conservative 1; Mismatches 0; Indels 0;
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Full-length cDNA libraries and normalization
Unpublished
Contact: Genoscope
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clone CS0DI012YM11 5-PRIME, mRNA sequence.
AL544923
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AL544923/c
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BX463747/c
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BX338865/c
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On Feb 15, 2001 this sequence version replaced g1:12888058.
Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr. Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 629.f For
more information about this cluster, see
http://www.genoscope.cns.fr.
http://www.genoscope.cns.fr.
Feng Liang Email: fliangolifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSDDI056BBI1QPI.
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the CENVSPORT 6 vector. Library was normalized.

276 c 226 g 257 t 58 others
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                                                                                                                 /organism="Homo sapiens"
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sites of the pCMVSPORT 6 vector. Library was normalized.
a 212 c 238 g 227 t 2 cthers
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COT 25-NORMALIZED Homo sapiens CDNA
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1. (bases 1 to 1060)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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  Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ Invitroden Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODI005BE03QPI. Location/Qualifiers
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Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 21.6; DB 13; Length 933;
Pred. No. 3.7e+02;
1; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALSE0767 Homo sapiens PLACENTA COT 25-NORM clone CS0DI056YC22 5-PRIME, MRNA sequence. ALSE0767
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/mol_type="mRNA"
/db_xref="taxon:9606"
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95.5%;
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Best Local Similarity 95.5
Matches 21; Conservative
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Best Local Similarity

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COT 25-NORMALIZED Homo sapiens CDNA
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCWNSPORT 6 vector. Library was normalized."
a 276 c 314 g 250 t 37 others
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BP 191 91006 EVRY cedex - France
BEMail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5957.f For
nore information about this cluster, see
http://www.genoscope.cns.fr/
egi-bin/cluster.egi?seq=CSOD1064DD02QP1&cluster=5957.f. Contact :
Feng Liang Email: fliang@ilfetech.com WRL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOD1064DD02QP1.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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                                                                                                                                                                                                                                                                        BX338865 Homo sapiens PLACENTA COT 25-NORN
clone CSODI064YH04 5-PRIME, mRNA seguence.
BX338865
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/mol type="mRNA"
/db xref="taxon:9606"
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                                                                                                      19
                                                                                                            CWGCTTTTTTGTACAACTTGT
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BX463747.1 GI:31031557
                                                       4 CAGCITITITIGIACAAACIIGI
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Conservative
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Contact: Genoscope
Genoscope
Genoscope
Genoscope
Bp 19106 EVRY Cedex - France
Bp 191 91006 EVRY Cedex - France
Inhitrogen. This sequence belongs to sequence cluster 1734.r. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi7seq-CS0DF072DD09QP1kcluster=1734.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
Feng Liang Email : fliang@lifetech.com URL :
http://tulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF027DD09QP1.
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/dev_stage="fetal"
/dev_stage="fetal"
/dev_stage="fetal"
/clone_lib="Momo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCWVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and Ecoxy sites of the pCMVSPORT 6 vector. Library was not normalized."

a 21 c 216 g 276 t l others
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                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 897)
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Genoscope - Centre National de Sequencage
Genoscope - Centre Carace
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 sequence cons.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 334.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI005BE03QPl&cluster=334.r. Contact
                                                                                                                                         Li.W.E., Gruber, C., Jessee, J. and Polayes, D.
Li.W.E., Gruber, C., Jessee, J. and Normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12801847
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF027YH18"
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21; Conservative
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Homo sapiens (human)
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BX333971 Homo sapiens NEUROBLASTOWA COT 50-NORWALIZED Homo sapiens CDNA clone CSODD004YN23 5-PRIME, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

    (bases 1 to 894)

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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BMail: sequefogenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9435.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
egi-bin/cluster.cgi?seq=CS0DD004CG12QP1&cluster=9435.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DD004CG12QP1.
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the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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                                                                                                                    Score 21.8; DB 13;
Pred. No. 3.1e+02;
0; Mismatches 2;
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AL538354.2 GI:31262948
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1 Similarity 92.0%;
23; Conservative (
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Library was not normalized." 7 others
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BX422399 Homo sapiens FETAL LIVER Homo sapiens CDNA clone
CSODM004YD15 5-PRIME, mRNA sequence.
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MRNA linear EST 22-MAY-2003
BAK477051 Homo sapiens THYMUS Homo sapiens CDNA clone CSOCAP005YP02
5-PRIME, MRNA sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 973)
                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 956)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAPOO5DHO1QPl&cluster=6437.r. Contact
cgi-bin/cluster.cgi?seq=CSOCAPOO5DHO1QPl&cluster=6437.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAPOO5DHO1QPl.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                  Contact: Genoscope
Genoscope - Centre National de Sequencage
BE 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invirrogen. This sequence belongs to sequence cluster 6437.r For
more information about this cluster, see
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
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                                                                                                                                                                                                                                                                           Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
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  BX457051/c
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vector. Library was not normalized."

vector. Library was not normalized."
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Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 BVRX cedex - France
BP 191 91006
France information about this cluster, see
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
France France Genoscope sequence ID : CSOASO09ZC07QPI.

Contaction/Qualifiers
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Invitrogen. This sequence belongs to sequence cluster 7228.f For more information about this cluster, see
http://www.gencoope.cns.ft/
cgi-bin/cluster.cgi?eq=CSODMO4CB08OP1&cluster=7228.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODMO04CB08QP1.

Location/Qualifiers
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Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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BX428996 Homo sapiens B CELLS (RAMOS CELL LINE) Homo sapiens CDNA
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10-NORWALIZED"
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Pred. No. 3.1e+02;
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
It, Mases 1 to 1201)
It, W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
Library was constructed by Life Technologies, a division of
thithin about this cluster. se
http://www.genoscope.cns.fr/
egi-bin/cluster.cgl?seq=CSODJ001DC06QP1&cluster=7763.r. Contact :
Feng Liang Email : fliang@alifetech.com URL :
http://tulllength.livitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODJ001DC06QP1.
                                                                         Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6911.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODC019BC08QP1&cluster=6911.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODC019BC08QP1.
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100.0%; Pred. No. ...
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BX361644.1 GI:30366552
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                           Contact: Genoscope
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nes 22; Conservative
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AL519260 Homo sapiens NEUROBLASTOMA Homo sapiens CDNA clone CSODA012YH14 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3874.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODA012DD07QP1&cluster=3874.r. Contact :
http://fullength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODA012DD07QP1.
Inter-1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcWvSPORT 6 vector. Library was normalized.
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Thill-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12782753
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - Prance
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
1 (bases 1 to 914)
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EST 05-MAY-2003

FEATURES

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mRNA linear EST 13-MAY-2003
A COT 25-NORMALIZED Homo sapiens
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/clone lib="Homos sapiens PRACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a Not1-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCWVSPORT 6 vector. Library was normalized."
268 c 207 t 58 others
                                                                                                                                                                                                                         BX359829 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CSODI062YC23 5-PRIME, mRNA sequence.
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BP 191 91006 EVRY cedex - France
Librally was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6269.r For
http://www.genoscope.ors.fr/
cgi-bin/cluster.cgi?seq=CSODI062AD12QP1&cluster=6269.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI062AD12QP1.
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Li W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1. (bases 1 to 1092)
1. ("I.", H.", Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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/db_xref="taxon:9606"
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                                                                                 35 CAGCITITIGIACAACTIGI
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BX394655/c
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Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EWRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2850.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi/seq-CSODF014BA04QP1&cluster=2850.r. Contact :
Feng Liang Email: fliang@lifetech.com URL :
http://fullnangh.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF014BA04QP1.
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(Gone lib="Homo sapiens FETAL BRAIN"

/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA

was primed with a NotI-oligo(dT) primer. Five prime end

enriched, double-strand cDNA was digested with Not I and

cloned into the Not I and EcoRV sites of the pCMVSPORT 6

cloned into the Not normalized."

233 c 278 g 189 t 1 others
                                                                                                                      /mol_type="mRNA"

/db xref="taxon:9606"

/db xef="taxon:9606"

/db xef="taxon:9608"

/clone="CS0DD005YC15"

/tissue type="mRUROBLASTOMA COT 50-NORNALIZED"

/clone_lib="Homo sapiens NEUROBLASTOMA con sapiens NeuroBlastoma 
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 934)
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Faraday Avenue Genoscope sequence ID : CSOBAK021BF12NM1.
Location/Qualifiers
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100.0%; Pred. No. 2.6e+02;
live 0; Mismatches 0; Indels
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/db_xref="taxon:9606"
/clone="CSODF014YA08"
/tissue_type="FEFAL BRAIN"
                                                                                                  /organism="Homo sapiens"
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95.8%;
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Matches 22; Conservative
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Best Local Similarity
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FEATURES

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BX329816
BX329816 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens CDNA clone CSODD005YC15 3-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 996)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAK021BF12NM1&cluster=4354.f. Contact
cgi-bin/cluster.cgi?seq=CSOBAK021BF12NM1&cluster=4354.f. Contact
Feng Liang Email : flitedefector.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex - France
Email: SequeGenoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4354.f For
more information about this cluster, see
                                                            AL550767
BX338865
BX463747
                                                                                    AL554923
AL554071
BX363509
BX386369
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BX463202
BX373155
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BX441089 BX441089
BX359829 BX359829
BX394655 BX394655
                                                     November 6, 2003, 22:08:13; Search time 1093.75 Seconds (without alignments) 555.531 Million cell updates/sec
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      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                22781392 segs, 12152238056 residues
                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                        1 gttcagcttttttgtacaaacttgt 25
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Listing first 45 summaries
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gb_gssl:*
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EST 02-MAY-2003

BX418181 BX418181 AL520832 AL520832 BX367104 BX367104

BX403441 BX403441

ALIGNMENTS

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comprising one or more mutated att recombination sites comprising at least one mutated att recombination sites comprising at least one mutated att recombination sites comprising at recombination in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination are used for the recombinational acid molecules. They can be used for changing vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cloaving fusion rags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning; (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
```

Sequence 204 BP; 80 A; 35 C; 31 G; 58 T; 0 other;

Gaps 0: Score 23.4; DB 21; Length 204; Pred. No. 0.73; 0; Mismatches 1; Indels 0; 1 GTTCAGCTTTCTTGTACAAGTTGT 25 93.6%; 24; Conservative Query Match Best Local Similarity Matches à

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184 GTTCAGCTTTTTGTACAAACTTGT 160

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AAC55476 standard; DNA; 204 BP RESULT 40 AAC55476/c 

AAC55476;

(first entry) 11-JAN-2001 Destination vector pDEST11 fragment nucleotide sequence.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda

Synthetic

WO200052027-A1.

08-SEP-2000.

02-MAR-2000; 2000WO-US05432

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC.

Cheo Hartley JL, Brasch MA, Temple GF,

ä

WPI; 2000-543948/49.

Isolated mucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 13; Fig 31; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB2, attB1, attB2, attB1, and attR2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated catt recombination site that interacts with the mutated att recombination are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracelular locations, cleaving fusion tags from the present sequences, constructing genes for fusion proteins, cleaning copy number, changing replicons, cloning into phages and cloning (I), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. 

Sequence 204 BP; 60 A; 53 C; 50 G; 41 T; 0 other;

Gaps . 0 93.6%; Score 23.4; DB 21; Length 204; 96.0%; Pred. No. 0.73; ive 0; Mismatches 1; Indels 0; Conservative Similarity 24; Query Match Local Matches

ö

181 Gricagcriririgracaaacrigr 157 1 GITCAGCITICITGIACAACTIGI 25 à du Search completed: November 6, 2003, 22:26:29 Job time : 112.5 secs

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mutated attraccombination site and a second muclaic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (1), (11), (111), primers, vectors and methods att recombination site. (1), (11), (111), primers, vectors and methods from the present invention are used for the recombinational cloning of muclaic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking muclaic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (1), (11), (111), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
                        comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the
recombination site; and (2) an isolated nucleic acid molecule (III)
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Sequence 153 BP; 50 A; 28 C; 40 G; 35 T; 0 other;

ö Gaps ô Length 153; 1; Indels Score 23.4; DB 21; Pred. No. 0.71; 0; Mismatches Query Match 93.6%; Best Local Similarity 96.0%; Matches 24; Conservative

à

AAC55465 standard; DNA; 204 BP RESULT 38 AAC55465, 

(first entry) 11-JAN-2001 AAC55465;

Destination vector pDEST6 fragment nucleotide sequence #1.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda

Synthetic.

WO200052027-A1.

38-SEP-2000

02-MAR-2000; 2000WO-US05432.

99US-0122389. 99US-0126049. 99US-0136744. 28-MAY-1999; 02-MAR-1999; 23-MAR-1999;

(LIFE-) LIFE TECHNOLOGIES INC.

Cheo D; Temple GF, Brasch MA, Hartley JL,

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL12, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 15; Fig 26; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att

recombination site; and (2) an isolated nucleic acid molecule (III)
comprising one or more mutated att recombination sites comprising at
least one mutation in its core region that enhances the efficiency of
recombination between a first nucleic acid molecule comprising the
mutated att recombination site and a second nucleic acid molecule
comprising a second recombination site that interacts with the mutated
att recombination site. (1), (III), primers, vectors and methods
from the present invention are used for the recombinational cloning of
nucleic acid molecules. They can be used for changing vectors, targeting
gene products to intracellular locations, cleaving fusion tags from
gene products to intracellular locations, cleaving fusion tags from
cleasired proteins, operably linking nucleic acid molecules of interest
clanding copy number, changing replicons, cloning into phages and
cloning (1), (III), (III), host cells and vectors can be used in the
production of polypeptides and antibodies. The present sequence is
used in the exemplification of the present invention. ö Gaps 0 Score 23.4; DB 21; Length 204; Pred. No. 0.73; Indels .. H Sequence 204 BP; 70 A; 40 C; 46 G; 48 T; 0 other; 0; Mismatches Query Match 93.6%; Best Local Similarity 96.0%; Matches 24; Conservative ( %\$ à

166 GirchGeriririgiachadarigi 142 25 1 GTTCAGCTTTCTTGTACAAACTTGT dd

AAC55470/c RESULT 39

AAC55470 standard; DNA; 204

AAC55470;

(first entry) 11-JAN-2001 Destination vector pDEST8 fragment nucleotide sequence.

Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda. Synthetic.

VO200052027-A1

38-SEP-2000

02-MAR-2000; 2000WO-US05432. 

99US-0126049. 99US-0136744. 99US-0122389 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC.

ä Cheo Brasch MA, Temple GF, Hartley JL,

WPI; 2000-543948/49.

attB2, attP1, attP2, useful for the Isolated nucleic acid molecules encoding an attBl, attLl, attL2, attRl, and attR2 nucleotide sequence recombinational cloning of polypeptides -

Example 15; Fig 28; 459pp; English

encoding an attB1, attB2, attB1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att The present invention describes isolated nucleic acid molecules (I)

```
recombination site; and (2) an isolated nucleic acid molecule (III)
comprising one or more mutated att recombination sites comprising at
least one mutation in its core region that enhances the efficiency of
recombination between a first nucleic acid molecule comprising the
mutated att recombination site and a second nucleic acid molecule
comprising a second recombination site that interacts with the mutated
att recombination site. (I), (II), primers, vectors and methods
from the present invention are used for the recombinational cloning of
nucleic acid molecules. They can be used for changing vectors, targeting
gene products to intracellular locations, classing vectors and
essired proceins, operably linking nucleic acid molecules of interest to
regulatory genetic sequences, constructing genes for fusion proteins,
changing copy number, changing replicans, cloning into phages and
cloning: (I), (II), (III), host cells and vectors can be used in the
production of polypeptides and antibodies. The present sequence is
used in the exemplification of the present invention.
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Sequence 125 BP; 61 A; 18 C; 14 G; 32 T; 0 other;

ö Gaps 0; Score 23.4; DB 21; Length 125; Pred. No. 0.69; 0; Mismatches 1; Indels 0; 93.6%; 96.0%; Local Similarity 96.0 Query Match Matches

GIICAGCITICITGIACAACIIGI 25 25 gricagciririrgiacaaacirgi 1

à B RESULT 36 AAC55485/ 

BP AAC55485 standard; DNA; 153

AAC55485;

11-JAN-2001 (first entry)

Destination vector pDEST15 fragment nucleotide sequence #2.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda

Synthetic

WO200052027-A1.

08-SEP-2000

02-MAR-2000; 2000WO-US05432.

99US-0126049. 99US-0122389. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC.

Ö, Cheo Temple GF, Brasch MA, WPI; 2000-543948/49. Hartley JL,

Disclosure; Fig 35; 459pp; English.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attB1, attB2, attB1, and attR2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att

recombination site; and (2) an isolated nucleic acid molecule (III)

comprising one or more mutated att recombination sites comprising at
least one mutation in its core region that enhances the efficiency of
recombination between a first nucleic acid molecule comprising the
mutated att recombination site and a second nucleic acid molecule
comprising a second recombination site and a second nucleic acid molecule
att recombination site. (1), (III), primers, vectors and methods
att recombination site. (1), (III), primers, vectors and methods
from the present invention are used for the recombinational cloning of
nucleic acid molecules. They can be used for changing vectors, targeting
gene products to intracellular locations, cleaving fusion tags from
desired proteins, operably linking nucleic acid molecules of interest to
regulatory genetic sequences, constructing genes for fusion proteins,
changing copy number, changing replicons, cloning into phages and
cloning. (1), (III), (III), host cells and vectors can be used in the
production of polypeptides and antibodies. The present sequence is
used in the exemplification of the present invention. 

Seguence 153 BP; 52 A; 29 C; 33 G; 39 T; 0 other;

· 0 Gaps 0; 93.6%; Score 23.4; DB 21; Length 153; 96.0%; Pred. No. 0.71; ive 0; Mismatches 1; Indels 0; Local Similarity 96.0 Query Match Best Loca Matches

à g

AAC55488/ RESULT

BP AAC55488 standard; DNA; 153

AAC55488;

(first entry) 11-JAN-2001 Destination vector pDEST16 fragment nucleotide sequence #2

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda.

Synthetic.

WO200052027-A1.

08-SEP-2000

02-MAR-2000; 2000WO-US05432.

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999;

28-MAY-1999;

(LIFE-) LIFE TECHNOLOGIES INC.

ä Cheo GF, Temple Brasch MA, Hartley JL,

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Disclosure; Fig 36; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att

ce interaction between the recombination site and a second att
recombination site; and (2) an isolated nucleic acid molecule (III)
comprising one or more mutated att recombination sites comprising at
least one mutation in its core region that enhances the efficiency of
recombination between a first nucleic acid molecule comprising the
mutated att recombination site and a second nucleic acid molecule
comprising a second recombination site that interacts with the mutated
att recombination site. (1), (II), (III), primers, vectors and methods
from the present invention are used for the recombinational cloning of
nucleic acid molecules. They can be used for changing vectors, targeting
gene products to intracellular locations, cleaving fusion tags from
desired proteins, operably linking nucleic acid molecules of interest to
regulatory genetic sequences, constructing genes for fusion proteins,
changing copy number, changing replicons, cloning into phages and
cloning. (1), (II), (III), host cells and vectors can be used in the
production of polypeptides and antibodies. The present sequence is
used in the exemplification of the present invention. 

Sequence 102 BP; 37 A; 24 C; 19 G; 21 T; 1 other;

Query Match 93.6%; Score 23.4; DB 21; Length 102; Best Local Similarity 96.0%; Pred. No. 0.68; Matches 24; Conservative 0; Mismatches 1; Indels 0 1 GITCAGCITICITGIACAACTIGI 25 셤

ö

Gaps

; 0

Grrcascrirrirgiacaacrist 68

AAC55453 standard; DNA; 120 BP AAC55453/c RESULT 34 

AAC55453;

(first entry) 11-JAN-2001 Irc expression cassette for destination vector pDEST1.

Bacteriophage lambda, att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda Escherichia coli.

WO200052027-A1.

08-SEP-2000

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-2000; 2000WO-US05432. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999;

(LIFE-) LIFE TECHNOLOGIES INC

Cheo D; Temple GF, Brasch MA, Hartley JL,

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the attL1, attL2, attR1, and attR2 nucleotid recombinational cloning of polypeptides

Disclosure; Fig 21; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB2, attL1, attL2, attR1, and attR2 nuclectide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity

comprising one or more untered and a second addition site, and (2) an isolated nucleic acid molecule all comprising one or more mutated attractomation sites comprising at least tone mutation its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising the mutated comprising a second recombination site that interacts with the mutated att recombination site. (1), (11), (111), primers, vectors and methods from the present invention are used for the recombinational cloning of runcleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, clanding of tusion rags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning (1), (11), (111), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. of interaction between the recombination site 

Sequence 120 BP; 44 A; 19 C; 28 G; 29 T; 0 other;

Gaps ; Length 120; Indels DB 21; 1; Score 23.4; DB Pred. No. 0.69; 0; Mismatches 73.6%; Local Similarity 96.0%; nes 24; Conservative Query Match Matches

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RESULT 35 AAC55384/

AAC55384 standard; DNA; 125

AAC55384;

(first entry) 11-JAN-2001 Recombination site nucleotide sequence attR1.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda.

VO200052027-A1.

32-MAR-2000; 2000WO-US05432 38-SEP-2000. 

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999;

28-MAY-1999;

(LIFE-) LIFE TECHNOLOGIES INC.

Cheo Brasch MA, Temple GF, Hartley JL,

ä

WPI; 2000-543948/49.

attP2, Isolated nucleic acid molecules encoding an attB1, attB2, attP1, a attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Claim 1; Fig 9; 459pp; English.

encoding an attB1, attB2, attP1, attP2, attL1, attL12, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att The present invention describes isolated nucleic acid molecules (I)

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recombination site, and (2) an isolated molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first mudele caid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, rargeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to
                                                                                                                                                                                                                                                                                                                                                                  regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning: (1), (11), (11), (11), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
of interaction between the recombination site and a second att
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 102 BP; 40 A; 22 C; 18 G; 22 T; 0 other;
      % X G G G G G G G G G G G G G G G X & G
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Score 23.4; DB 21; Length 102; Pred. No. 0.68; 1; Indels 0; Mismatches 1 GTTCAGCTTTCTTGTACAACTTGT 25 83 GTTCAGCTTTTTGTACAACTTGT 59 93.6%; 24; Conservative Query Match Best Local Similarity Matches 24; Conserv

; 0

Gaps

; 0

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AAC55508 standard; DNA; 102 BP AAC55508; 

(first entry) 11-JAN-2001 Destination vector pDEST24 fragment nucleotide sequence #1.

Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda Synthetic

WO200052027-A1.

08-SEP-2000.

02-MAR-2000; 2000WO-US05432

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC

Cheo D; Hartley JL, Brasch MA, Temple GF,

WPI; 2000-543948/49

attPl, a for the Isolated nucleic acid molecules encoding an attB1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence useful recombinational cloning of polypeptides -

Example 5; Fig 44; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB2, attL1, attL2, attL1, attL2, attL1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising on or more att recombination sites comprising at least one mutation in its core region that increases the specificity

cerombination between the recombination site and a second at the recombination site; and (2) an isolated mucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting generated proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning into phages and cloning into phages and artibodies. The present sequence is production of polypeptides and artibodies. The present sequence is ., The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attL1, attL2, attL1, attLR2 and attR2 nucleide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2 nuclectide sequence useful for the recombinational cloning of polypeptides -Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; Gaps ó DB 21; Length 102; Destination vector pDEST25 fragment nucleotide sequence #1. 1; Indels recombination site and a Sequence 102 BP; 37 A; 25 C; 19 G; 21 T; 0 other; mutant; recombinational cloning; entry vector; de gene product targeting; fusion tag cleavage; ds. Cheo D; Score 23.4; DB Pred. No. 0.68; 0; Mismatches 71 GITCAGCITICITGIACAAACTIGI 25 Temple GF, 95 gircagciriririgiacaaacrigi Example 5; Fig 45; 459pp; English. ВЪ (LIFE-) LIFE TECHNOLOGIES INC 99US-0122389. 99US-0126049. 99US-0136744. 93.6%; 96.0%; 5511/c AAC55511 standard; DNA; 102 02-MAR-2000; 2000WO-US05432 (first entry) Brasch MA, 24; Conservative interaction between Bacteriophage lambda. WPI; 2000-543948/49. Similarity WO200052027-A1. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; Hartley JL, 11-JAN-2001 08-SEP-2000. Synthetic. AAC55511; Query Match Local Matches RESULT 33 AAC55511/ 

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comprising one or more mutated att recombination sites comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first mucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site (1), (II), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from cegulatory genetic sequences, constructing genes for fusion proteins, changing replicons, cloning into phages and cloning. (I), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
recombination site and a second att
of interaction between the
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Sequence 102 BP; 35 A; 19 C; 20 G; 28 T; 0 other;

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..
0
93.6%; Score 23.4; DB 21; Length 102; 96.0%; Pred. No. 0.68;
                           Indels
                            1,
                            0; Mismatches
                                                      1 GTTCAGCTTTCTTGTACAAACTTGT 25
                                                                       GTTCAGCTTTTTTGTACAAACTTGT 46
                            24; Conservative
              Best Local Similarity
  Query Match
                            Matches
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Gaps

AAC55500 standard; DNA; 102 11-JAN-2001 AAC55500; AAC55500/c RESULT 30 

BP.

(first entry)

Destination vector pDEST21 fragment nucleotide sequence #2.

Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda

Synthetic.

40200052027-A1. 08-SEP-2000 02-MAR-2000; 2000WO-US05432

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC

Cheo D; Temple GF, Brasch MA, Hartley JL,

WPI; 2000-543948/49.

attP2, Isolated nucleic acid molecules encoding an attB1, attB2, attP1, a attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Disclosure; Fig 41; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attL1, attB2, attB1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity

encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleit caid observed (II) comprising one or more att recombination sites comparising at least one mutation in its core region that increases the specificity

The present invention describes isolated nucleic acid molecules (I)

Example 5; Fig 43; 459pp; English.

attP1, a for the

Isolated nucleic acid molecules encoding an attBl, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence useful recombinational cloning of polypeptides -

ö of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at recombination its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site and is econd nucleic acid molecule att recombination site. (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion lasg from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, regulatory genetic sequences. Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds. Gaps changing copy number, changing replicons, cioning into phages and cloning. (I), (II), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. . 0 Score 23.4; DB 21; Length 102; Pred. No. 0.68; Destination vector pDEST23 fragment nucleotide sequence #1. Indels Sequence 102 BP; 45 A; 13 C; 24 G; 20 T; 0 other; ۲; Cheo D; 0; Mismatches 1 GITCAGCITICITGIACAAACITGI 25 58 Hartley JL, Brasch MA, Temple GF, 82 Gricagcrirrirgracaaacrigr BP (LIFE-) LIFE TECHNOLOGIES INC 99US-0122389. 99US-0126049. 99US-0136744. 93.6%; 32-MAR-2000; 2000WO-US05432. AAC55505 standard; DNA; 102 (first entry) Ouery Match
Best Local Similarity 96.0' Sacteriophage lambda. WPI; 2000-543948/49. 40200052027-A1 12-MAR-1999; 23-MAR-1999; 28-MAY-1999; 11-JAN-2001 08-SEP-2000 Synthetic. AAC55505; RESULT 31 AAC55505, d \$ à

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recombination between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising the comprising a second recombination site that interacts with the mutated att recombination site in (III), primers, vectors and methods trompt the present invention are used for the recombinational cloning of rucleic acid molecules. They can be used for changing vectors, targeting ene products to intracellular locations, cleaving fusion tags from captuatory genetic sequences, constructing genes for fusion proteins, changing copy number. Changing replicons, cloning into phages and cloning: (III), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Seguence 87 BP; 26 A; 19 C; 21 G; 21 T; 0 other;
                   5555555555555555555555555
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Score 23.4; DB 21; Length 87; Pred. No. 0.67; Indels .. H 0; Mismatches 1 GITCAGCITICITGIACAAACTIGI 25 55 79 Gricagcririridiacaaacricr 1 Similarity 96.0%; 24; Conservative 93.6%; Query Match Best Local Similarity Matches 셤

AAC55497 standard; DNA; 95 RESULT 28

BP

(first entry) 11-JAN-2001 AAC55497;

Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; attL; attL; geneant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds. Destination vector pDEST20 fragment nucleotide sequence #2. 

Bacteriophage lambda. Synthetic

WO200052027-A1.

08-SEP-2000

02-MAR-2000; 2000WO-US05432

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999;

TECHNOLOGIES INC. (LIFE-) LIFE Cheo D; Brasch MA, Temple GF, Hartley JL,

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 23; Fig 40; 459pp; English

encoding an attB1, attB2, attP1, attL2, attL1, attL2, attR1, and attR2 mucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity present invention describes isolated nucleic acid molecules (I)

recombination between the recombination site and a second att
recombination site; and (2) an isolated nucleic acid molecule (III)
comprising one or more mutated att recombination sites comprising at
least one mutation in its core region that enhances the efficiency of
recombination between a first nucleic acid molecule comprising the
mutated att recombination site and a second nucleic acid molecule
comprising a second recombination site that interacts with the mutated
att recombination site. (1), (III), (III), primers, vectors and methods
from the present invention are used for the recombinational cloning of
nucleic acid molecules. They can be used for changing vectors, targeting
quene products to intracellular locations, cleaving fusion tags from
desired proteins, operably linking nucleic acid molecules of interest to
regulatory genetic sequences, constructing genes for fusion proteins,
changing copy number, changing replicons, cloning into phages and
cloning (1), (III), host cells and vectors can be used in the
production of polypeptides and antibodies. The present sequence is
used in the exemplification of the present invention. \$

Sequence 95 BP; 41 A; 13 C; 15 G; 26 T; 0 other;

Gaps ; Length 95; Indels DB 21; 93.6%; Score 23.4; DB 96.0%; Pred. No. 0.68; 0; Mismatches Local Similarity 96.0 Query Match Matches

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g

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Gaps

.; 0

RESULT 29 AAC55458/

BP AAC55458 standard; DNA; 102

AAC55458;

(first entry) 11-JAN-2001 GST expression cassette for destination vector pDEST3 #2.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda Escherichia coli

WO200052027-A1.

08-SEP-2000

02-MAR-2000; 2000WO-US05432.

99US-0126049. 99US-0136744. 99US-0122389. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; 

(LIFE-) LIFE TECHNOLOGIES INC.

Cheo D; Temple GF, Brasch MA, Hartley JL,

WPI; 2000-543948/49.

isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 15; Fig 23; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attL1, attL2, attR1, and attR2 nuclectide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity

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AASO6174-AASO6322 represent Bacteriophage lambda att recombination site nucleic acid sequences, and PCR primers of the invention. The att sequences are recognised by the recombination protein lambda integrase (Int). The invention is a new method of producing a population of hybrid nucleic acids comprising mixing at least a first population of nucleic acids comprising one or more recombination sites with at least one target nucleic acid comprising one or more recombination sites and causing some or all of the nucleic acids to recombine with all or some of the target nucleic acids. The method is useful for producing a population of hybrid nucleic acids which may be the same or different. The nucleic acids may also be used to express therapeutic proteins or peptides and they acids may also be used to create novel fusion proteins by expressing different sequences linked to each other. The method allows simultaneous cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Destination vector pDEST22 fragment nucleotide sequence #2.
                                                                                                                                                                                                                                                                                                                  ch 33.6%; Score 23.4; DB 22; Score 23.4; DB 22; Score 24; Conservative 0; Mismatches 1:
                                                                                                                                                                                                                                                                                        Sequence 43 BP; 20 A; 5 C; 11 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                            1 GITCAGCITICITGIACAACTIGI 25
                                                                                                                                                                                                                                                                                                                                                                                                                 29 GTTCAGCTTTTTTGTACAAACTTGT 5
                                                                                                                                                                                                                                                            two or more different nucleic acids.
          Example 7; Page 209; 357pp; English
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99US-0126049.
99US-0136744.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC55503 standard; DNA; 82 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-2000; 2000WO-US05432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-543948/49.
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC55503;
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 26
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The present invention describes isolated nucleic acid molecules (I)

Disclosure; Fig 42; 459pp; English.

Cheo D;

Temple GF,

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or interaction between the recommination sites also a second of recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated attrecombination sites comprising at comprising one or more mutated attrecombination site sites the efficiency of least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated attrecombination site and a second nucleic acid molecule comprising a second recombination site and a second nucleic acid molecule comprising a second recombination site, [1], (III), primers, vectors and methods attrecembination site. [1], (III), primers, vectors and methods attrement invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, classing vectors, targeting gene products to intracellular locations, classing vectors, targeting center proteins, operably linking nucleic acid molecules of interest centaring copy number, changing replicons, cloning into phages and clanning (1), (III), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is production of polypeptides and antibodies. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attL1, attL2, attL1, and attR2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attF2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage lambda; att; recombination site; attB; attR; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .
interaction between the recombination site and a second att
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Destination vector pDEST27 fragment nucleotide sequence #2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 23.4; DB 21;
Pred. No. 0.67;
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 82 BP; 39 A; 16 C; 17 G; 10 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GITCAGCITICITGIACAAACTIGI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                70 GricaGcrirririciacaAAcrici 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 47; 459pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  93.6%;
96.0%;
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99US-0136744.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC55517 standard; DNA; 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriophage lambda
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-543948/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   828888888888888888888888
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Length 43;

present invention describes isolated nucleic acid molecules (I)

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02-MAR-2000; 2000WO-US05432.
                                                         23-MAR-1999;
28-MAY-1999;
                                                    08-SEP-2000
                                 a
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The invention relates to improving the production of a secondary

metabolite by a fungus. This involves modulating the expression of at

metabolite by a fungus. This involves modulating the expression of at

least one ZBC (Zinc binuclear cluster protein) gene in a manner to

improve the yield of the secondary metabolite. Methods of the invention

improve the yield of the secondary metabolite e.g.

artibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such

as lovastin or mevastatin), an immunosuppressant (such as cyclosporin A),

an ergot alkaloid (such as ergotamine), an angiogenesis inhibitor (such

as ovalicin), a glucan synthase inhibitor, glictoxin family of compounds,

a fungal toxin, a modulator of cell surface receptor signalling, a plant

compound. The method results in a decrease in fermentor run-time, a

decrease in the size of the fermentor required for the production of

decrease in the size of the secondary metabolite, or a decrease in the

compounds of vectors the production, which translates into decreased

construction of vectors containing the SEC genes of the invention.

In records ABLS8887-ABLS8598 represent primers that are used in

construction of vectors containing the SEC genes of the invention.

Note: The sequence data for this patent did not form part of the printed

specification, but was obtained directly from WIPO at

the productor.

Compounds of the production of the printed

specification, but was obtained directly from WIPO at
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DB 24; Length 35; 1; Indels Sequence 35 BP; 14 A; 7 C; 7 G; 7 T; 0 other; Score 23.4; DB Pred, No. 0.61; 0; Mismatches 1 GTTCAGCTTTCTTGTACAACTTGT 25 93.64; Query Match Best Local Similarity وههدر المحالة المحا

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Gaps

; 0

GTTCAGCTTTTTTGTACAAACTTGT 11 35

AAC55545 standard; DNA; 43 (first entry) att site PCR primer attRl 11-JAN-2001 AAC55545;

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; PCR primer; ss.

Bacteriophage lambda Synthetic.

WO200052027-A1.

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999;

(LIFE-) LIFE TECHNOLOGIES INC

Cheo Temple GF, Brasch MA, Hartley JL,

Ä

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 19; Page 142; 459pp; English.

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condition a attB1, attB2, attB2, attB1, attB2, attB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR primer attR1 used to produce a population of hybrid DNA molecules.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 43 BP; 20 A; 5 C; 11 G; 7 T; 0 other;
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09-MAR-2000; 2000US-0188020.
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24; Conservative
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TEMPLE G F.
HARTLEY J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacteriophage lambda
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20-OCT-1999; 99US-0160587.
19-JAN-2000; 2000US-0487558.
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Norman T, B
E, Zhang L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (MICR-) MICROBIA INC.
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Milne T,
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AAH19591/c
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The present sequence is a primer which was used in an example illustrating an invention relating to a method for improving production of a secondary metabolite by a fungus. The method involves modulating the expression of a gene involved in the regulation of secondary metabolite production. The gene may be modulated in a manner that increases the yield or productivity of metabolite, increases the yield or productivity of metabolite, increases ceffects or competing metabolites, alters the characteristics of the effects or competing metabolites, alters the production of the metabolite, causes conditional lysis of the fungus, or increases the resistance of the fungus to deleterious effects of exposure to the resistance of the fungus to deleterious effects of exposure to the secondary metabolite. The method is useful for producing genetically modified fungi, which are useful for producing secondary metabolites such as antibacterial compounds,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antihypercholesterolaemic compounds, immunosuppressants, modulators of cell surface receptor signalling, plant growth regulators, pigments, insecticides or anti-neoplastic compounds. The present sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          used in the preparation of clones to regulate secondary metabolite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 35 BP; 14 A; 7 C; 7 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GITCAGCTTTCTTGTACAACTTGT 25
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                               Example 1; Page 67; 139pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         th 93.6%;
Similarity 96.0%;
24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             production
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ABL58593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 23
ABL58593/
à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          셤
                                                                                                                                                    chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods insertion of heterologous DNA into plant artificial chromosomes, methods isolated plant artificial chromosomes methods isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous mucleic acid encoding a gene product such as enzymes, antisense RNA, KNA, FNA, FNA, Encutural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and cytokines, growth factors, antisense, blood factors, antisens, harmones, cytokines, growth factors, antisense, herbicides, or stress in a plant. The heterologous mucleic acid optionally encodes a product that provides an estimate use and/or improves the nutrient quality of the plant. The nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid optionally encodes a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (PAC). This producing plant artificial chromosome (YAC). This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Secondary metabolite production, gene expression modulation, genetically modified fungus; antibacterial; antihypercholesterolaemic; immunosuppresent; cell surface receptor signalling; pigment; plant growth regulator; insecticide; anti-neoplastic; ccdB; death gene; pEZC7201; PCR primer; ss.
                                                                                                                                   The invention relates to a novel method for producing plant artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.6%; Score 23.4; DB 25; Length 25; 96.0%; Pred. No. 0.59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid pEZC7201 ccdB cassette PCR oligo MO511.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GITCAGCITICITGIACAACTIGI 25
                                                                 Disclosure; Page 262; 269pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
   nucleic acids
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Gaps

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Length 35; Indels

Score 23.4; DB 22; Pred. No. 0.61; 0; Mismatches 1;

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Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein; antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastin; mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine; angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; glictamitican synthase inhibitor; glictamitican synthase inhibitor; glictamitican synthase inhibitor; glictamiticans transference receptor; plant growth regulator; pigment; insecticide; antineoplastic; PCR; primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New method for improving the production of a secondary metabolite e.g. antineoplastic agent, ergot alkaloid from a fungus involves modulation of the expression of at least one zinc binuclear cluster protein gene
                                                                                                                                                                                                                                                                                                                                                                                                                            Sherman A;
                                                                                                                                                                                                                                                                                                                                                                                                                              Maxon M,
 BP
                                                                                                                                                                                                                                                                                                                                19-SEP-2001; 2001WO-US29288.
                                                                                                                                                                                                                                                                                                                                                                 19-SEP-2000; 2000US-233564P.
ABL58593 standard; DNA; 35
                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            Madden K,
                                                                                                                                                                                                                                                                                                                                                                                             (MICR-) MICROBIA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-352005/38.
                                                                                                                                                                                                                                                                                                                                                                                                                            Holtzman D,
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Example 1; SEQ ID 7; 49pp + sequence listing; English.

Maxon M;

Cali B, Hecht P, Holtzman D, Madden K, Royer J, Salama S, Sherman A, Silva J; , Mayorga M, Feibelman T;

Improving production of secondary metabolite by fungus, for producing proteins of interest, involves modulating the expression of gene involved in regulation of secondary metabolite production

WPI; 2001-374304/39.

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Esposito D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-MAY-2001; 2001US-294687P. 04-JUN-2001; 2001US-296329P.
                                                    Li X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABT16628 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fabijanski SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Conservative
(INVI-) INVITROGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGRISOMA INC
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                                                    Cheo D,
                                                                                                     WPI; 2003-129436/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200296923-A1.
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                                                      Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Perez C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABT16628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nvention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (AGRI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed innegarian in the presence of chromosome, and permits site-directed innegarian in the presence of lambda-integrase. Also described: (I) a platform artificial chromosome expression system (ACES) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (MI) for introducing a heterologous nucleic acid into a platform artificial chromosome, preferably an ACES. (II) is useful for introducing a heterologous nucleic acid molecule into a platform or a trificial chromosome, preferably an ACES. (II) is useful for producing a ranspenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection, by a carrier system, microinjection, microcall fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for maxing a library of ACES comprising random portions of a genome. ACC44612 to ACC44132 and ABPS6650 to ABPS6657 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ô
                                                                                                                                                                                                                                                                                                                   Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                             ы
                                                                                                                                                                                          Fleming
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93.6%; Score 23.4; DB 25; Length 25; 96.0%; Pred. No. 0.59; cive 0; Mismatches 1; Indels (
                                                                                                                                                                               Perez C, Lindenbaum M, Greene A, Leung J, Shellard J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
                                                                                                                                         (CHRO-) CHROMOS MOLECULAR SYSTEMS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 43; Page 143; 272pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-2002; 2002WO-US15947
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                                                            30-MAY-2001; 2001US-294758P
21-MAR-2002; 2002US-366891P
             30-MAY-2002; 2002WO-US17452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABZ58734 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 96.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                          WPI; 2003-140461/13.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAY-2003
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                                                                                                                                                                                             Perkins E,
Stewart S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Н
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                             interest
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                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid with a second population; (c) mixing the second population of nucleic acid with a second population; (c) mixing the second population or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid molecules acid molecules to selecting and isolating nucleic acid molecules. Sequences ABZ58727-762 represent att recombination site sequences used in the method of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant artificial chromosome; PAC; transgenic plant; vaccine;
blood factor; herbicide; stress; agronomical; nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
                                                                                                                                                                                                          the second
                                                                                                                                                          Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the secon population of nucleic acid with a second target nucleic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Artificial plant chromosome related oligo SEQ ID No 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 23.4; DB 25;
Pred. No. 0.59;
Byrd DRN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHROMOS MOLECULAR SYSTEMS INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perkins E;
                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 13A; 273pp; English.
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first expression cassette, comprising a first promoter operably linked to a nucleic acid sequence encoding a syncytium-inducing polypeptide (such as a fusogenic membrane glycoptotein) and flanked on either side by a sequence recognised by a recombinase, and/or a second expression cassette comprising a tumour-specific promoter operably linked to a nucleic acid sequence encoding a recombinase. The nucleic acid of the first expression cassette may be linked to a hypoxic response element (HRE), the second expression cassette may contain a promoter linked to a nucleic acid encoding a cytokine, and a third cassette may contain a tumour specific promoter linked to tumour specific promoter linked to the nucleic acid encoding the recombinase. The tumour
                                                                                                                                                                                                                                                                                                                                                                                        Recombinant nucleic acid vector for reducing tumour size, has expression cassette comprises a promoter linked to nucleic acid sequence encoding a syncytium-inducing polypeptide and flanked on either side by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specific promoter is, for example, a carcinoembryonic antigen (CEA) promoter or a tyrosinase promoter and the recombinase is, for example, Cre recombinase or FLP recombinase. The invention is useful for reducing tumour size by administering the compositions as retroviral vectors, or in a cell containing the vector, to an individual in need of treatment for a disease caused by malignant cells. This sequence represents an Int recombinase site core region attnR2, required for excisive recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention relates to a recombinant nucleic acid vector comprising a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 25 BP; 5 A; 5 C; 4 G; 10 T; 1 other;
                                                                                                                                                                                                                                                       (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 42; 84pp; English.
                                                                                                                                                                30-MAR-2001; 2001WO-US10250.
                                                                                                                                                                                                           31-MAR-2000; 2000US-193977P.
                                                                                                                                                                                                                                                                                                        Harrington K,
                     Bacteriophage lambda.
                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-656985/75.
                                                                      WO200174861-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinase
                                                                                                                    11-OCT-2001
                                                                                                                                                                                                                                                                                                        Vile RG,
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Murphy S, Bateman A;

Gaps ; 0 Length 25; Indels Score 23.4; DB 23; Pred. No. 0.59; 1; 0; Mismatches 25 1 GTTCAGCTTRCTTGTACAAACTTGT 1 GIICAGCITICITGIACAACTIGI 93.6%; Query Match Best Local Similarity 96.0 Matches 24; Conservative ð

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ABQ82121 standard; DNA; 25 BP 11-DEC-2002 (first entry) ABQ82121; RESULT 18 

Core sequence of recombination site attR1 SEQ ID NO:4.

Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ss.

Synthetic

WO200259294-A1

01-AUG-2002.

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The present interaction to be considered by the fragments having:

(a) Selectable marker region capable of being expressed in the recipient cell, preferably in bacteria such as Escherichia coli;

(b) Selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (ii) promoter or expressed in the recipient cell; and court recombination sites by RNA polymerases of a cutaryoric cell or by prokaryoric RNA polymerases of and pourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryoric cell. The first and fourth recombination sites, or the second and third recombination sites, and preferably are identical. The first and second recombination site, and preferably are identical. The first and second recombination site, or the third and fourth recombination sites, do not recombine for other or with a same recombination site, and other or with a same recombination site. The vector is useful for the convert a DNA fragment into an inverted repeat structure. Plants of transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same conventional breeding scheme to produce more plants with the same convention of the core sequence of recombination site attBl which is given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes a vector (I) comprising operably linked
                                                                                                                                                                                                                                                       New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.6%; Score 23.4; DB 24; Length 25; 96.0%; Pred. No. 0.59; ive 0; Mismatches 1; Indels C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the present invention.
                                                                                                                      (CSIR ) COMMONWEALTH SCI & IND RES ORG.
                                                                                                                                                                      Helliwell C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25
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                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 14; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GITCAGCTITCTTGTACAAACTIGT
24-JAN-2002; 2002WO-AU00073.
                                             26-JAN-2001; 2001US-264067P.
29-NOV-2001; 2001US-333743P.
                                                                                                                                                                      Waterhouse P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 Similarity 96.0
24; Conservative
                                                                                                                                                                                                                    WPI; 2002-682669/73.
                                                                                                                                                                      Wesley S,
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Best Local
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Gaps

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ACC44658 standard; DNA; 25 ACC44658; RESULT 19 ACC44658

BP.

Recombination site related oligonucleotide SEQ ID NO:49. (first entry) 29-MAY-2003

Chromosome, based platform; artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; PCR primer; ss.

Synthetic

WO200297059-A2. 

05-DEC-2002.

25

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In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host
                                                                                                          Recombination site; cloning; att; ss.
GTTCAGCTTTTTGTACAAACTTGT
                                                                                                                                                                                                          (LIFE-) LIFE TECHNOLOGIES INC.
                                              AAF55743 standard; DNA; 25
                                                                            (first entry)
                                                                                           Recombination site attR1
                                                                                                                                                                                                                         Hartley JL, Brasch MA;
                                                                                                                                                                                                                                        WPI; 2001-136877/14.
                                                                                                                        Unidentified
                                                                                                                                        US6171861-B1
                                                                                                                                                                     12-JAN-1998;
                                                                                                                                                                                    07-JUN-1996;
                                                                                                                                                                                            07-JUN-1995;
                                                                             12-APR-2001
                                                                                                                                                       09-JAN-2001
                                                              AAF55743;
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96US-0663002. 95US-0486139. 98US-0005476

ö The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors ach comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture; and selecting for a host comprising the chimeric nucleic acid molecule, and selecting gainst a host comprising the vectors comprising the second vector, to clone the nucleic acid. The present sequence is a recombinantion site, which may be used in the method of the present Gaps ö 93.6%; Score 23.4; DB 22; Length 25; 96.0%; Pred. No. 0.59; ive 0; Mismatches 1; Indels 0 Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other; Claim 25; Column 46; 73pp; English. 24; Conservative Local Similarity Query Match Matches à

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Lambda phage Int recombinase site core region DNA sequence attnR2.
                       25
                                        25
                        1 GIICAGCIIICIIGIACAAACIIGI
                                       Gricaderirririatacaaacirdr
                                                                                     BP
                                                                                   AAS14785 standard; DNA; 25
                                                                                                                       27-FEB-2002 (first entry)
        Conservative
Local Similarity
        24;
                                                                                                       AAS14785;
        Matches
                                                                     RESULT 17
                                                                            AAS14785
                                                                                      염
                          ð
                                                                                1 GTICAGCTITCTTGTACAACTIGT 25
                                                                                          AAC87874 standard; DNA; 25 BP
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Core region; recombination site; cloning; chimeric DNA; characteristic; mutation; att site; lox site; ss.

Escherichia coli

JS6143557-A

07-NOV-2000

99US-0233493. 20-JAN-1999; 96US-0663002. 07-JUN-1996;

98US-0005476 L2-JAN-1998;

95US-0486139 17-JUN-1995;

(LIFE-) LIFE TECHNOLOGIES INC.

Brasch MA, Hartley JL;

WPI; 2001-049004/06.

ø Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank selectable marker and comprise a core region having an engineered mutation

Claim 1; Column 18; 73pp; English.

The present invention describes an isolated nucleic acid molecule (I) comprising a first nucleic acid sequence having a defined sequence comprising a first nucleic acid sequence having a defined sequence (AACB7866 to AACB7866 to AACB7881, or an RNA sequence corresponding to AACB7866 to AACB7881. Also described are: (I) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site that removes one or more stop codons from the being an att or lox site; (2) an isolated nucleic acid molecule (III) comprising a first att recombination site comprising a mutation that comprising a first att recombination site comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids or (IV). The nucleic acids are used in comprising the above mentioned sites suitable for subcloning reactions. The use of nucleic acids for DNA or RNA subcloning reactions. The use of nucleic acids for DNA or RNA subcloning, highly specific, rapid, and less labour intensive. 

Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Gaps . 0 Length 25; Indels 93.6%; Score 23.4; DB 22; 96.0%; Pred. No. 0.59; iive 0; Mismatches 1; Query Match

ö

Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine; syncytium-inducing polypeptide; fusogenic membrane glycoprotein; tumour; recombinase; tumour-specific promoter; hypoxic response element; HRE; ss; tyrosinase promoter; Cre; FLP; retroviral vector; malignant cell; cancer; cytostatic; gene therapy; Int recombinase site core region; attnR2; excisive recombination.

Escherichia coli core region recombinant site attR1 SEQ ID NO:9.

(first entry)

02-MAR-2001

AACB7874
ID AAC
XX
AC AAC
XX
DT 02-1
XX
XX
XX

AAC87874;

RESULT 16

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site-specific recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the VDMs, thereby producing one or more desired product molecules (PMS). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that make the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention.
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Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

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Gaps
                                     ô
      Length 25;
                                     Indels
ch 93.6%; Score 23.4; DB 20; Similarity 96.0%; Pred. No. 0.59; 24; Conservative 0; Mismatches 1:
                                                                  1 GITCAGCITICITGIACAACTIGT 25
                                                                                               25
                                                                                               GTTCAGCTTTTTTGTACAACTTGT
   Query Match
Best Local Similarity
Matches 24; Conserv
                                                                                                셤
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ö

RESULT 13

AAD14437 standard; DNA; 25 (first entry) 01-NOV-2001 AAD14437; 

BP.

Recombination site attB3 DNA

Recombination site; copy number; replicon; recombinatorial cloning; attB3; dB.

Unidentified

US6270969-B1

07-AUG-2001

99US-0233492 20-JAN-1999; 96US-0663002. 95US-0486139. 07-JUN-1996;

(INVI-) INVITROGEN CORP.

Brasch MA; Hartley JL,

WPI; 2001-488248/53.

Methods for apposing nucleic acids comprising an expression signal an a gene/partial gene, using recombinatorial cloning by incubating the nucleic acids in the presence of a recombination protein under conditions for recombination.

Claim 14; Column 18; 76pp; English.

The invention relates to a method for apposing an expression signal and a gene or partial gene, using recombinatorial cloning. The method incubates nucleic acids comprising the expression signal and the gene/partial gene in the presence of a recombination protein under conditions sufficient to cause recombination and therefore appose the expression signal and the gene or partial gene. The methods are useful for apposing an expression signal and a gene or partial gene using recombinatorial cloning. The methods are also useful for changing vectors, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages, and cloning e.g., For products (with an attB site at one end and a loxp site at the other end), genomic DNAs, and cDNAs. The methods are highly specific, rapid, and less labour intensive than before the combination site that the chart and a loxp present sequence is a recombination site. useful for recombination cloning

Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

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AASO6174-AASO6322 represent Bacteriophage lambda att recombination site nucleic acid sequences, and PCR primers of the invention. The integrace (Int). The invention is a new method of producing a population of hybrid nucleic acids comprising mixing at least a first population of nucleic acids comprising mixing at least a first population of nucleic acids comprising one or more recombination sites with at least causing some or all of the nucleic acids to recombination sites and causing some or all of the nucleic acids to recombine with all or some of the target nucleic acids. The method is useful for producing a population of hybrid nucleic acids which may be the same or different. The nucleic acids which may be the same or different. The nucleic acids may be used to express therapeutic proteins or peptides and they may also be used to create novel fusion proteins by expressing different sequences linked to each other. The method allows simultaneous cloning of
                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Producing hybrid nucleic acids, useful for expressing novel therapeutic polypeptides, by mixing the same or different nucleic acids having one or more recombination sites in the presence of recombination proteins,
                                                                                                                                                                                                                                                                                                               Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
                                              Gaps
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0
             Length 25;
                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Byrd DRN;
              22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hartley JL,
             DB
.59;
                                            0; Mismatches
             Score 23.4;
Pred. No. 0.
                                                                                                                                                                                                                                                                                    Phage-lambda recombination site attR1.
                                                                           25
                                                                                                         Gricagciririrgiacaaaciigi 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Fig 24A; 357pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 two or more different nucleic acids.
                                                                                                                                                                                                                                                                                                                                lambda integrase; therapeutic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Temple GF,
                                                                                                                                                                                        ВЪ
              93.6%;
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09-MAR-2000; 2000US-0188020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-2000; 2000WO-US33546.
                                                                                                                                                                                        AAS06181 standard; DNA; 25
                                                                                                                                                                                                                                                    (first entry)
Ouery Match
Best Local Similarity 96...
Best Local 24; Conservative
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BRASCH M A.
TEMPLE G F.
HARTLEY J L.
BYRD D R N.
                                                                                                                                                                                                                                                                                                                                                              Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-356174/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brasch MA,
                                                                             1 GTTCAGCT
                                                                                                                                                                                                                                                                                                                                                                                             WO200142509-A1.
                                                                                                                                                                                                                                                    12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUN-2001
                                                                                                                                                                                                                       AAS06181;
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(BRAS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HART/)
(BYRD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TEMP/)
                                                                                                                                                        RESULT 14
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24; Conservative

Matches

8

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Gaps

. 0

Indels

7 DB 22;

Length 25;

Score 23.4; DB Pred. No. 0.59; 0; Mismatches

93.6%;

Query Match Best Local Similarity

therapeutic

Byrd DRN;

Temple GF, Hartley JL,

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AASO6174-AASO6322 represent Bacteriophage lambda att recombination site nucleic acid sequences, and PCR primers of the invention. The att sequences are recognised by the recombination protein lambda integrase (Int). The invention is a new method of producing a population of hybrid nucleic acids comprising an exceptionation sites with at least one target nucleic acid comprising one or more recombination sites with at least one target nucleic acid comprising one or more recombination sites and of the target nucleic acids. The method is useful for producing a population of hybrid nucleic acids which may be the same or different. The nucleic acids which may be the same or different. The nucleic acids which may be the same or different. The nucleic acids which may be the same or different is acids may also be used to exapte novel fusion proteins by expressing different sequences liked to each other. The method allows simultaneous cloning of
                                                                                                                                                                                                                Producing hybrid nucleic acids, useful for expressing novel therapeutic polypeptides, by mixing the same or different nucleic acids having one or more recombination sites in the presence of recombination proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               att recombination site; core region; mutation; enhance; recombination;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 43 BP; 19 A; 5 C; 12 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                vector; subcloning; regulation; exchange; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  two or more different nucleic acids.
                                                                                                                                                                                                                                                                                             Example 7; Page 209; 357pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GITCAGCITICITGIACAAACTIGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            29 GITCAGCITICITGTACAACTIGT
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              99US-0169983
                           09-MAR-2000; 2000US-0188020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT48218 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hartley JL;
                                                                        BRASCH M A.
TEMPLE G F.
                                                                                                         HARTLEY J L.
                                                                                                                                                       Brasch MA,
                                                                                                                                                                                    WPI; 2001-356174/37
                                                                                                                         BYRD D R N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   attR1 core region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9640724-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-1996;
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                10-DEC-1999;
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(TEMP/)
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                                                            (CHEO/)
                                                                                                          HART/)
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О
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         à
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Gaps

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Length 43; 0; Indels

100.0%; Score 25; DB 22; 100.0%; Pred. No. 0.12; iive 0; Mismatches 0;

25

BP.

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core region has at least one engineered mutation that enhances recombination in vitro in the formation of a Cointegrate or Product DNA. These core regions can be incorporated into novel vector donor DNA molecules. The nucleic acids, vectors and methods of the invention are used to obtain chimeric nucleic acid using recombination proteins and engineered recombination sites in vitro or in vivo. The improved specificity, speed and yields of the invention facilitates DNA or RNA subcloning, regulation or exchange useful for any related purpose, e.g. in vitro recombination of DNA segments, and in vitro or in vivo insertion or modification of transcribed, replicated, isolated or genomic DNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to movel methods for cloning or subcloning one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     more nucleic acid molecules (NAMs) comprising: (a) combining in vitro o in vivo: (1) at least one insert donor molecules (IDMs) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMs) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or more
                                                                                                                                    AAT48210-25 are att recombination site core region DNA sequences. The
                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                         o'
                                       Nucleic acids, vectors and methods to obtain chimeric nucleic using recombinant proteins and engineered recombination sites vitro or in vivo
                                                                                                                                                                                                                                                                                                                                                                                       Score 23.4; DB 18; Length 25; Pred. No. 0.59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning; donor; recombination site; vector; chimeric; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oligonucleotide #9 for recombination and cloning method.
                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hartley JL, Temple GF;
                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GITCAGCITICITGIACAACTIGT 25
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                                                                                                          Claim 14; Page 55; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New nucleic acid cloning methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (LIFE-) LIFE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP.
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97US-0065930.
                                                                                                                                                                                                                                                                                                                                                                                            93.68;
                                                                                                                                                                                                                                                                                                                                                                                                            96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                           24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-303011/25.
            WPI; 1997-065168/06.
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-OCT-1998;
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24-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9921977-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX78943;
                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
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attP2,

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30-MAY-2001; 2001US-294687P.
      30-MAY-2002; 2002WO-US17451
                                                                                                                                                                                                               11-JAN-2001 (first entry)
                                                                                                                                                                                                                      att site PCR primer attR2.
                                   Perez C, Fabijanski SF,
                                                                                                                                                                                                                                           Bacteriophage lambda
                                          WPI; 2003-140436/13
                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                      WO200052027-A1.
                                                                                                                                                                                                                                                             08-SEP-2000.
05-DEC-2002,
                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                       AAC55546;
                         CHRO-)
                            (AGRI-)
                                                                                                                                                                                            Matches
                                                                                                                                                                                         RESULT 9
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mutated attracombination site and a second muclaic acid molecule comprising a second recombination site that interacts with the mutated attracombination site. (I), (II), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion range from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleotide sequence. Also described are: (1) an isolated nucleic acid nucleotide sequence. Also described are: (1) an isolated nucleic acid nucleotide sequence. Also described are: (1) an isolated nucleic acid an eleast of it comprising one or more attracombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and second attracombination site; and (2) an isolated nucleic acid molecule (III) comprising one mutated attracombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR primer attR2 used to produce a population of hybrid DNA molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes isolated nucleic acid molecules (I)
                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1 nucleotide sequence useful for the recombinational cloning of polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 21; Length 4:
100.0%; Pred. No. 0.12; '. rw:-marches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 43 BP; 19 A; 5 C; 12 G; 7 T; 0 other;
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                                                                                                                                                                                                       Cheo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GITCAGCITICITGIACAACTIGT 25
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                                                                                                                                                                                                                                                                                                                                                                                                           Example 19; Page 142; 459pp; English.
                                                                                                                                                                                                         Temple GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29 GITCAGCITTCTTGIACAAACITGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lambda integrase; therapeutic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP.
                                                                                                                                                       (LIFE-) LIFE TECHNOLOGIES INC.
                                                     99US-0122389.
                                                                                                    99US-0136744
02-MAR-2000; 2000WO-US05432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS06218 standard; DNA; 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity lou..
Local Similarity lou..
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                                                                                                                                                                                                         Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriophage lambda
                                                                                                                                                                                                                                                         WPI; 2000-543948/49.
                                                     02-MAR-1999;
                                                                            23-MAR-1999;
28-MAY-1999;
                                                                                                                                                                                                         Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS06218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS06218/
     g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial diromosomes. The involves into plant artificial diromosomes. The solated plant artificial chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, ERNA, structural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and copromised proteins, vaccines, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that provides an agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The chromosome (BAC) or a yeast artificial chromosome (YAC). This producing plant artificial chromosomes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                         Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                               CHROMOS MOLECULAR SYSTEMS INC. AGRISOMA INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 262; 269pp; English
                                                                                                                                                                                                                                                                    Perkins E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAC55546 standard; DNA; 43 BP
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Gaps

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11-DEC-2000; 2000WO-US33546.

WO200142509-A1 14-JUN-2001.

Length 43;

30-MAY-2002; 2002WO-US17452. 30-MAY-2001; 2001US-294758P. 21-MAR-2002; 2002US-366891P.

WO200297059-A2

05-DEC-2002.

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The present interaction describes a vector of the present interaction allowing replication in a recipient cell, preferably in bacteria such as Escherichia coll; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or cell; and (c) a chimeric DNA construct comprising: (i) promoter or cell; and polymerases of a cukaryotic cell or by prokaryotic RNA polymerases of a chimer dourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites; (iii) 3' transcription terminating sites are capable of reacting with a same recombination site, and correct capable of reacting with a second recombination site, and the third and fourth recombination sites, don't recombination site. The vector is useful for the third and fourth recombination site. The vector is useful for convert a DNA fragment into an investment structure. Plants convert a DNA fragment into an investment or subset in a recombination or subset in a subset of the convert a DNA fragment into an investment or subset in a result of the convert a DNA fragment into an investment or subset in a result of the convert a DNA fragment into an investment or subset in a present investment in a present i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents the core sequence of recombination site attBl which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 present invention describes a vector (I) comprising operably linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA -
                                                                                                                                                                                                                                                                                                             (CSIR ) COMMONWEALTH SCI & IND RES.ORG.
                                                                                                                                                                                                                                                                                                                                                                              Wesley S, Waterhouse P, Helliwell C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 14; 104pp; English.
                                                                                                                                  24-JAN-2002; 2002WO-AU00073.
                                                                                                                                                                                                       26-JAN-2001; 2001US-264067P.
                                                                                                                                                                                                                                        29-NOV-2001; 2001US-333743P
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WO200259294-A1.
                                                                 01-AUG-2002
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Gaps . 0 100.0%; Score 25; DB 24; Length 25; 100.0%; Pred. No. 0.12; ive 0; Mismatches 0; Indels Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other; GITCAGCITICITGIACAACTIGI 25 1 GTTCAGCTTTCTTGTACAAACTTGT 25 25; Conservative Query Match Best Local Similarity 셤

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ACC44659 standard; DNA; 25 29-MAY-2003 ACC44659; RESULT 7

BP.

Recombination site related oligonucleotide SEQ ID NO:50.

(first entry)

Chromosome-based platform, artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; PCR primer; ss.

WO200296923-A1.

Unidentified.

Synthetic.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (I) a platform artificial chromosome expression system (Aces) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (MI) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for introducing a heterologous nucleic acid molecule into a platform artificial artificial chromosome, preferably an Aces. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachmid, or mammall) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinjection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell, preferably a stem cell or an embryo. (II) comprises a heterologous muchies acid that encodes a therapeutic product which is useful for making a library of Aces comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                      Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                           Perez C, Lindenbaum M, Greene A, Leung J, Fleming E; Shellard J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.1
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exemplification of the present invention.
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                                                                                                                                                                                         (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 43; Page 143; 272pp; English.
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                                                                                                                                                                                                                                                                                                WPI; 2003-140461/13.
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                                                                                                                                                                                                                                    Perkins E,
Stewart S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                           interest
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Plant artificial chromosome; PAC; transgenic plant; vaccine; blood factor; herbicide; stress; agronomical; nutrient quality; bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC; Artificial plant chromosome related oligo SEQ ID No 41. ABT16629 standard; DNA; 25 (first entry) 03-APR-2003 ABT16629; **ABT16629**  m

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The present invention describes an isolated nucleic acid molecule (I) comprising a first nucleic acid sequence having a defined sequence (AAC87886 to AAC87881, sequences complementary to AAC87886 to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87881. Also described are: (1) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site to avoids hairpin formation, the recombination site of an isolated nucleic acid molecule (III) comprising a first att recombination site comprising a first att recombination site comprising a mutation that above mentioned nucleic acids; and (4) relis comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids or (IV). The nucleic acids are used in mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining engineered recombination in vitro or in vivo makes the methods for DNA or RNA subcloning, highly specific, rapid, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank a selectable marker and comprise a core region having an engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 22; Length 25;
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                    Core region; recombination site; cloning; chimeric DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Core sequence of recombination site attR2 SEQ ID NO:5.
                                           characteristic; mutation; att site; lox site; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 22
100.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Column 18; 73pp; English
                                                                                                                                                                                                                                                                                                                                                  LIFE-) LIFE TECHNOLOGIES INC.
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                                                                                                                                                                                                                                                         96US-0663002,
98US-0005476,
95US-0486139.
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                                                                                                                                                                                                                                                                                                                                                                                           Hartley JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   less labour intensive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-049004/06.
                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                  12-JAN-1998;
07-JUN-1995;
                                                                                                                                                                                                                   20-JAN-1999;
                                                                                                                                                                                                                                                            07-JUN-1996;
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                                                                                                                            US6143557-A
                                                                                                                                                                        07-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                           Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mutation
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors ach comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture; and selecting for a host comprising the chimeric nucleic acid mixture, and selecting for a host comprising the chimeric nucleic acid molecule, and selecting against a host comprising the vectors comprising the second vector; to clone the nucleic acid. The present sequence is a recombinantion site, which may be used in the method of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli core region recombinant site attR2 SEQ ID NO:10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 5 A; 5 C; 4 G; 11 T; 0 other;
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                                                                                                                                                                                                                                                                                                                             Recombination site; cloning; att; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 25; Column 46; 73pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LIFE-) LIFE TECHNOLOGIES INC.
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95US-0486139.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hartley JL, Brasch MA;
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Best Local Similarity
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                                                                                                                                                                                              AAF55744;
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Matches
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Gaps

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g 8

5 A; 5 C; 4 G; 11 T; 0 other;

BP;

Sequence 25

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vitro or in vivo
                                                                                        26-OCT-1998;
                                                                                            23-OCT-1998;
                                                                                              24-OCT-1997;
                                                                 17-AUG-1999
                                                                                 WO9921977-A1
                                                                                    06-MAY-1999
                                                                                                      Brasch MA,
                                                                             Synthetic.
                                    Query Match
                                                             AAX78944
                                        Matches
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have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention.
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                                                                                  AAT48210-25 are att recombination site core region DNA sequences. The core region has at least one engineered mutation that enhances recombination in vitro in the formation of a Cointegrate or Product DNA. These core regions can be incorporated into novel vector donor DNA molecules. The nucleic acids, vectors and methods of the invention are used to obtain chimeric nucleic acid using recombination proteins and engineered recombination sites in vitro or in vivo. The improved specificity, speed and yields of the invention facilitates DNA or RNA subcloning, regulation or exchange useful for any related purpose, e.g. in vitro recombination of DNA segments, and in vitro or in vivo insertion or modification of transcribed, replicated, isolated or genomic DNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMs) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or more sites which do not recombine with each other; and (3) one or more site-specific recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the VDMs, thereby producing one or more desired product molecules (PMs). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or in vivo: (1) at least one insert donor molecules (IDMs) comprising one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 18; Length 25; 100.0%; Pred. No. 0.12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oligonucleotide #10 for recombination and cloning method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cloning; donor; recombination site; vector; chimeric; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTTCAGCTTTCTTGTACAAACTTGT
                                                Claim 14; Page 55; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hartley JL,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LIFE-) LIFE TECHNOLOGIES INC
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nes 25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Methods for apposing nucleic acids comprising an expression signal an a gene/partial gene, using recombinatorial cloning by incubating the nucleic acids in the presence of a recombination protein under conditions for recombination -
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                                                                                Gaps
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                                                                             0; Indels
                           Length
                      100.0%; Score 25; DB 20;
100.0%; Pred. No. 0.12;
iive 0; Mismatches 0;
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                                                                                                                                  1 GTTCAGCTTTCTTGTACAAACTTGT
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                                                                                                                                                                                                                                                                                                                     BP
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Query Match
Query Match
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                                                                                                                                                                                                                                                                    RESULT 3
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November 6, 2003, 21:05:38; Search time 111.5 Seconds (without alignments) 605.255 Million cell updates/sec
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                                                                                                                                                                                            5105512
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                          2552756 segs, 1349719017 residues
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Core sequence of r Recombination site Artificial plant c Recombination site Recombination site Escherichia coli c attR2 core region. Oligonucleotide #1 Description ABQ82122 ACC44659 ABT16629 AAX78944 AAD14438 AAF55744 AAC87875 AAT48219 

100.0

100.0

Nucleic acids, vectors and methods to obtain chimeric nucleic acid using recombinant proteins and engineered recombination sites in

WPI; 1997-065168/06.

att site PCR prime PCR primer attR2 u	region	de de		da reco	S	chia coli	la phage Int	О	1	Att site nucleotid	Artificial plant c	Plasmid pEZC7201 c	Oligonucleotide MO	att site PCR prime	CR primer at	Destination vector		ination	•~		Destination vector	estination	Destination vector	rc expression ca	ecombinatio	es	a)	estinat	estinat	estinati	is6	estinati	nat	estinat	estination vect	
AAC55546 AAS06218	321	394	143	18	AAF55743	AAC87874	8	212	ACC44658	ABZ58734	ABT16628	AAH19591	ABL58593	54	521	AAC55503	551	9	45	AAC55500	AAC55505	550	551	545	53	AAC55485	548	546	547	AAC55476	546	AAC55478	AAC55468	AAC55514	549	
21	18	20	22	22	22	22	23	24	25	25	25	22	24	21	22	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	
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255	~	÷	ň	~	'n	23.4	23.4	m	m	m	m	23.4	23.4	23.4	23.4	23.4	23.4	m	23.4	23.4	23.4	m	m	23.4	23.4	23.4	23.4	23.4	m	m	m	m	23.4	m	m	
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## ALIGNMENTS

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att recombination site; core region; mutation; enhance; recombination; vector; subcloning; regulation; exchange; ss.
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                                                                                                    AAT48219 standard; DNA; 25
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                                                                                                                                                                                                                                                                                                                                                                                                             attR2 core region.
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                                                                                                                                                                                                    AAT48219;
RESULT 1
AAT48219
                                                                                                                                                    THE STANDARD ```

PAT 16-AUG-2002

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Recombinational cloning using engineered recombination sites Patent: EP 1227147-A 8 31-JUL-2002; INVITROGEN CORPORATION (US)
   Query Match 88.0%; Score 22; DB 6; Length 25; Best Local Similarity 100.0%; Pred. No. 70; Matches 22; Conservative 0; Mismatches 0; Indels
                                       25 bp
Sequence 8 from Patent EP1227147.
AX491647.
AX491647.1 GI:22324155
   1. .25
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
   Search completed: November 6, 2003, 23:06:41
  Location/Qualifiers
   Hartley, J.L. and Brasch, M.A.
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Recombinational cloning using engineered recombination sites
Patent: US 6270969.A 8 07-AUG-2001,
Location/Qualifiers
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Hartley,J.L. and Brasch,M.A.

Recombinational cloning using engineered recombination sites

Patent: US 6171861-A 8 09-JAN-2001;

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Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.

Recombinational oloning using nucleic acids having recombination
Patent: JP 2002500861-A 16 15-JAN-2002;

LIFE TECHNOLOGIES INC
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PR 24-OCT-1998 JP 60/065930,23-OCT-1998 US 09/177387 PI JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC C12N15/09, C1204/68,C12N15/00
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Hartley,J.L. and Brasch,M.A.
Recombinational clouing using engineered recombination sites
Patent: US 6270969-A 16 07-AUG-2001;
   Vile, R.G., Harrington, K., Murphy, S. and Bateman, A. Compositions and methods for tissue specific gene regulation
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Hartley,J.L. and Brasch,M.A.
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Recombinational cloning using engineered recombination sites
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PAT 29-OCT-2001

FEATURES

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   Losses 1 to 13990)
Haag,J.R., Lee,D.W. and Aramayo,R.
Direct Submission
Submitted (27-40-2002) Biology, Texas A&M University, BSBW #415,
College Station, TX 77843-3258, USA
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   1 (bases 1 to 13990)
Haag, J.R., Lee, D.W. and Aramayo, R.
Description of a GATEMAY Destination Vector For High-Throughput
Construction of Neurospora crassa Histidine-3 (his-3)-Gene
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Lipoxygenase genes, promoters, transit peptides and proteins
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Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.
Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.
Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.
Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.
LIFE TECHNOLOGIES INC
   PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI JAMES L HARTLEY, MICHAEL A BRASCH,GARY F TEMPLE, DONNA K FOX PC C12N15/09,C12Q1/68,C12N15/00
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JOURNAL REFERENCE

TITLE JOURNAL

FEATURES

AUTHORS

DEFINITION ACCESSION VERSION KEYWORDS SOURCE

RESULT 20 AY196825 LOCUS

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PAT 24-JAN-2003
   Goossens, A. and Inz, D. The use of genes encoding membrane transporter pumps to stimulate the production of secondary metabolites in biological cells Patent: WO 02093888-A 9 24-0CT-2002, Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
  Unpublished
2 (pases 1 to 12677)
Griswold.C.M. Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
Direct Submission
Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, B.P. A toolkit for transformation and mutagenesis in Drosophila using
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   Unpublished
2 (bases 1 to 12677)
Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, E.P.
Direct Submission
Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC 27709, USA
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piggyBac transformation vector pB-UGIR w+
artificial sequences; vectors.
1 (bases 1 to 12677)
Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, E.P.
A toolkit for transformation and mutagenesis in Drosophila using
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BASE COUNT ORIGIN

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1 (bases 1 to 11005)
Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, B.P.
A toolkit for transformation and mutagenesis in Drosophila using
   Unpublished
2 (bases 1 to 11005)
Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
Briect Submission
Submitted (13-DBC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, N
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I (bases 1 to 11005)
Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
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2 (bases 1 to 11005)
Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
Direct Submission
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Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.
Direct Submission
Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
f.Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
Germany
  26.7.1733
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circular SYN 25-JUN-2002

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Binary vector pJawohl8-RNAi

(bases 1 to 9019)
Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.

(bases 1 to 9019)
Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.

Direct Submission
Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut

E. Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
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o a 1199 c 1279 g 1311 t
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  Plaetinck,G., Renard,J.P. and Bogaert,T. Vector constructs
Pactor: WO 01188121-A 10 22-NOV-2001;
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à g ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

JOURNAL

COMMENT

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Jakoby, M.J., Heim,M.A. and Weisshaar,B.
Use of a gateway compatible vector for transient plant transfection
Unpublished
   circular SYN 27-MAR-2003
  PAT 03-APR-2003
   VFO551314

4462 bp DNA circular SYN 27-MAR-
Transfection vector pBTdest.

AJ551314.

AJ551314.1 GI:29335742

amp gene; beta lactamase; cat gene; ccdB gene; chloramphenicol
acctyl transferase; control of cell death B protein.

Transfection vector pBTdest
Transfection vector pBTdest
Transfection vector pBTdest
artificial sequences; vectors.
   2 (bases 1 to 4462)
Jakoby,M.J.
Direct Submission
Submitted (26-MAR-2003) Jakoby M.J., Salamini, MPI for Plant
Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, GERMANY
Location/Qualifiers
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Patent: WO 02066653-A 63 29-AUG-2002;
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Patent: WO 0224865-A 9 28-MAR-2002;
Microbia, INC. (US)
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   PAT 29-MAR-2003
   BD131335 25 bp DNA linear PAT 18-SEP-2002 Recombinational cloning using nucleic acids having recombination
   ö
   Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
  (bases 1 to 25)
Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
Recombinational cloning using nucleic acids having recombination
Patent: JP 2002500861-A 9 15-JAN-2002;
LIFE TECHNOLOGIES INC
  OS UNILLOW...

BN JP 200250861-R/9

PD 15-JAN-2002

PP 24-OCT-1998 JP 2000518069

PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI

JAMES I HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC

C12N15/09,C12Q1/68,C12N15/00

CC Description of Unknown Organism: recombination products FH

Key Location/Qualifiers
  Holtzman,D., Madden,K., Maxon,M. and Sherman,A.
Modulation of secondary metabolite production by zinc binuclear
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PAT 26-SEP-2002
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  Hartley, J.L. and Brasch, M.A.
Recombinational cloning using engineered recombination sites
Patent: EP 1229113-A 9 07-AUG-2002;
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Vile,R.G., Harrington,K., Murphy,S. and Bateman,A.
Compositions and methods for tissue specific gene regulation
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  PAT 29-0CT-2001
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  PAT 17-0CT-2001
  PAT 16-MAY-2001
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  (bases 1 to 25)
Hartley, J.L. and Brasch, M.A.
Recombinational cloning using engineered recombination sites
Patent: 13 6270969-A 9 07-AUG-2001;
Location/Qualifiers
   1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
Hartley,J.L. and Brasch,M.A.
Facombinational cloning using engineered recombination sites
Patent: US 6171861-A 9 09-JAN-2001;
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

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l (bases 1 to 25)

Ratley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
Recombinational cloning using nucleic acids having recombination.

LIFE TECHNOLOGIES INC

OS Unknown

PN JP 2002500861-A/10

PD 15-JAN-2002;

PN JP 2002500861-A/10

PP 24-OCT-1998 US 09/177387 PI

PR 24-OCT-1999 US 06/065930,23-OCT-1998 US 09/177387 PI

JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DONNA K FOX PC

C12N15/09,C12Q1/68,C12N15/00

CC Description of Unknown Organism: recombination products FH

Key Location/Qualifiers

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FT Fource Location/Qualifiers

FT Fource Location/Qualifiers
  BD131336 25 bp DNA linear PAT 18-SEP-2002 Recombinational cloning using nucleic acids having recombination
  PAT 26-SEP-2002
  Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: EP 1229113-A 10 07-AUG-2002;
INVITROGEN CORPORATION (US)
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   PAT 16-AUG-2002
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   Recombinational cloning using engineered recombination sites Patent: EP 1227147-A 10 31-JUL-2002; INVITROGEN CORPORATION (US) Location/Qualifiers
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Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: W6 62709569-A 10 07-AUG-2001,
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| iption                        | 1881. Sequence 1882. Sequence 1882. Sequence 1883. Sequence 1883. Sequence 1883. Sequence 1883. Sequence 1883. Sequence 1884. | AX306327 Sequence |
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| SUMMARIES                     | AK1645<br>AK1245<br>AK4916<br>AK4916<br>AK26911<br>AK26911<br>AK26911<br>AK2691<br>AK408<br>AK408<br>AK408<br>AK196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX196<br>AX163<br>AX498<br>AX4981<br>AX4981<br>AX4981<br>AX4981                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 32                |
| *<br>Query<br>Match Length DB |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 5148              |
| Score                         | 44 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 5 21.8            |
| Result<br>No.                 | 0000 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | •                 |

## ALIGNMENTS

| PAT 16-MAY-2001    |            |                        |          |          |          |                   | 1,000                          | CTOIL STREET                                                 |                                      |                     |
|--------------------|------------|------------------------|----------|----------|----------|-------------------|--------------------------------|--------------------------------------------------------------|--------------------------------------|---------------------|
| linear             |            |                        |          |          |          |                   |                                | recompris                                                    |                                      |                     |
| AR124530 25 bp DNA |            | AR124530.1 GI:14109891 | •        | Unknown. | Unknown. | 1 (bases 1 to 25) | Hartley, J.L. and Brasch, M.A. | Recombinational cloning using engineered recombination sices | Patent: US 6171861-A 10 09-JAN-2001; | Location/Qualifiers |
| AR124530<br>LOCUS  | DEFINITION | VERSION                | KEYWORDS | SOURCE   | ORGANISM | REFERENCE         | AUTHORS                        | TITLE                                                        | JOURNAL                              | FEATURES            |

```
Search completed: November 7, 2003, 02:22:26 Job time : 103.25 secs
             Sequence 42, Application US/09855797A Patent No. US20020094574A1 GENERAL INFORMATION:
  TYPE: DNA
ORGANISM: Unknown
   g
  à
   RESULT 38
US-10-055-001A-26

Sequence 26, Application US/10055001A

Sequence 26, Application US/10055001A

Sequence 26, Application No. US20030049835A1

GENERAL INFORMATION:
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Wethod and means for producing efficient silencing constructs
TITLE OF INVENTION: Using recombinational cloning
FILE REFERENCE: HELIGA

CURRENT APPLICATION NUMBER: US/10/055,001A

CURRENT FILING DATE: 2002-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.1

SEQ ID NO 26

LENGHH: 17691
  Sequence 26, Application US/10055001A

Publication No US20030049835A1

GENERAL INFORMATION:

APPLICANT: Wealey, Susan V.

APPLICANT: Wealey, Stristopher A.

APPLICANT: Wealen's Helliukell, Christopher A.

TITLE OF INVENTION: Using recombinational cloning

FILE REPRENCE: HELICA

CURRENT APPLICATION NUMBER: US/10/055,001A

CURRENT FILING DATE: 2002-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn version 3.1

SSOFTWARE: PatentIn version 3.1

SEQ ID NO 26

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                           Gaps
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93.6%; Score 23.4; DB 14; Length 17681;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0;
  Query Match
93.6%; Score 23.4; DB 14; Length 17681;
Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches 1; Indels 0;
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US-10-055-001A-26
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Best Local Similarity 96.0%; Pred. No. 1.4;
Matches 24; Conservative 0; Mismatches
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   16879 GricaGCrititiciaCaaacrici 16903
  13050 GITCAGCTITITIGIACAACTIGT 13026
  1 GITCAGCTITCTIGIACAACTIGI 25
   1 GITCAGCTITCTTGTACAAACTIGT 25
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  TYPE: DNA ORGANISM: Artificial sequence
  TYPE: DNA
ORGANISM: Artificial sequence
  RESULT 39
US-10-055-001A-26/c
   FEATURE:
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RESULT 40

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APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Hartley, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: 0942.266.281
PRIOR PLILING DATE: 1999-04-22
PRIOR PPLICATION NUMBER: US 60/065,930
PRIOR PLILING DATE: 1999-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
  Gaps
  ; OTHER INFORMATION: Description of Unknown Organism: recombination; CTHER INFORMATION: products
US-09-855-797A-42
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  Indels
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   1 GITCAGCITICITGTACAACTIGT 25
   1 GTTCAGCTTTTTTTTACWAASTKGW 25
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Sequence 24, Application US/10055001A
Publication No. US20030049835A1
GENERAL INFORMATION
APPLICANT: Wesley, Susan V.
APPLICANT: Weterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs;
TITLE OF INVENTION: Using recombinational cloning
FILE REFERENCE: HELLGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
   US-10-055-001A-24

Sequence 24, Application US/10055001A

Sequence 24, Application US/10055001A

Sequence 24, Application US/10055001A

Sequence 24, Application US/10055001A

Sequence 24, Application No. US20030049835A1

GENERAL INFORMATION:

APPLICANT: Wesley, Susan V.

APPLICANT: Waterhouse, Peter A.

APPLICANT: Helliwell, Christopher A.

TITLE OF INVENTION: Using recombinational cloning

FILE REFRENCE: HELIGA

CURRENT APPLICATION NUMBER: US/10/055,001A

CURRENT FILING DATE: 2002-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn version 3.1

SEQ ID NO 24

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  Length 17476;
   Length 17476;
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   Indels
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Pred. No. 1.4;
   1;
  DB 12;
  ; OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24
  OTHER INFORMATION: acceptor vector phellsGate8
   Score 23.4; D
Pred. No. 1.4;
  0; Mismatches
   0; Mismatches
  Score 23.4;
   16674 Gricagcrirrirgiacaaacrigi 16698
   13050 GTTCAGCTTTTTTGTACAACTTGT 13026
   ; FEATURE:
; OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7
   1 GTICAGCITICITGIACAAACTIGI 25
   25
   1 GITCAGCITICITGIACAAACITGI
   93.6%;
96.0%;
  ch 93.6%;
1 Similarity 96.0%;
24; Conservative (
  ORGANISM: Artificial sequence
   TYPE: DNA ORGANISM: Artificial sequence
  93.6%;
  TYPE: DNA ORGANISM: Artificial
   Query Match
Best Local Similarity
   US-10-055-001A-24/c
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LENGTH: 17476
  US-10-055-001A-24
     SEQ ID NO 7
LENGTH: 17476
  Query Match
  IYPE: DNA
  FEATURE:
  FEATURE:
   Matches
   ð
   g
  ð
  Sequence 7. Application US/10385546
| Publication No. US20030175783A1
| Publication No. US20030175783A1
| Publication No. US20030175783A1
| GENERAL INFORMATION:
| APPLICANT: Waterhouse, Peter
| APPLICANT: Wesley, Suan
| APPLICANT: Helliwell, Chris
| APPLICANT: Webley, Suan
| APPLICANT: Helliwell, Chris
| TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
| TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
| TITLE OF INVENTION: WINBER: US/10/385,546
| CURRENT APPLICATION NUMBER: US/10/385,546
| PRIOR APPLICATION NUMBER: US/60363852
| PRIOR APPLICATION NUMBER: US/60363852
| PRIOR FILING DATE: 2003-03-14
| NUMBER OF SEQ ID NOS: 7
| SEQ ID NO 7
| LENGTH: 17476
  Sequence 7, Application US/10385546
Publication No. US20030175783A1
GENERAL INFORMATION:
APPLICANT: Waterhouse, Peter
APPLICANT: Wesley, Susan
APPLICANT: Welliwell, Chris
TITLE OF INVEXTION: Methods and means for monitoring and modulating gene silencing
FILE REFERENCE: COLINA-US2
CURRENT APPLICATION NUMBER: US/10/385,546
CURRENT PILIOR DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60363852
PRIOR APPLICATION NUMBER: US 60363852
PRIOR FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.0
TITLE OF INVENTION: Method and means for producing efficient silencing constructs FILE REFERENCE: BELLGA
FILE REFERENCE: BELLGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 25
LENGTH: 17458
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   Length 17458;
   ó
  Indels
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  OTHER INFORMATION: plasmid phellsdate 8
  25
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  1 GTTCAGCTTTCTTGTACAAACTTGT
   TYPE: DNA ORGANISM: Artificial sequence
   TYPE: DNA
ORGANISM: Artificial
  US-10-385-546-7/c
   US-10-385-546-7
  US-10-385-546-7
   Query Match
  FEATURE:
   FEATURE:
   Best Loca
Matches
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APPLICANT: Wesley, Susan V.
APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Weing recombinational cloning
FILE REFERENCE: HELLGA
CURRENT PEPLICANTON NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 25.5
   Gaps
   Gaps
  APPLICANT: Wang, X.
APPLICANT: Cooper, Bret
TITLE OF INVENTION: Promoters for regulation of plant expression
FILE OF INVENTION: Promoters
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2001-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 581
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  Score 23.4; DB 14;
Pred. No. 1.4;
0; Mismatches 1;
  Query Match 93.6%; Score 23.4; DB 10; Best Local Similarity 96.0%; Pred. No. 1.3; Matches 24; Conservative 0; Mismatches 1;
  ; OTHER INFORMATION: acceptor vector pHELLSGATE11
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   16656 Gricagcrirrirgiacaaacrigi 16680
   142 Gricagcrirrirgracaaacrigr 118
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   Sequence 25, Application US/10055001A Publication No. US20030049835A1 GENERAL INFORMATION:
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US-10-055-001A-25/c
Sequence 25, Application US/10055001A; Publication No. US20030049835A1; GENERAL INFORMATION:
   TYPE: DNA
, ORGANISM: Arabidopsis thaliana
US-09-887-576-581
  93.6%;
  TYPE: DNA ORGANISM: Artificial seguence
   Query Match
Best Local Similarity 96.0
Matches 24; Conservative
Brown, D.
Chang, H.
   Han, B.
                     Chang,
   17458
   RESULT 32
US-10-055-001A-25
   FEATURE:
   LENGTH:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOL
  ö
  Gaps
  .
0
   DB 14; Length 6464;
  Indels
  LOCATION: (4504)..(4941)
OTHER INFORMATION: flori (fl intergenic region)
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Pred. No. 1.2;
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                 FILE REFERENCE: 0942.5120001
CURRENT APPLICATION NUMBER: US/10/151,690
CURRENT FILING DATE: 2002-05-21
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR APPLICATION NUMBER: US 60/291,973
PRIOR PELING DATE: 2001-05-21
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn version 3.1
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Matches 24; Conservative
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ORGANISM: Artificial sequence
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LOCATION: (4104)..(4264)
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; LOCATION: (5340)..(6420)
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US-10-151-690-20
   NAME/KEY: gene
LOCATION: (273)..(393)
OTHER INFORMATION: attRl
  NAME/KEY: gene
LOCATION: (1994)..(2118)
OTHER INFORMATION: attR2
FEATURE:
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  . (3503)
  LOCATION: (1648)..(1953)
   LOCATION: (2598)..(3503
OTHER INFORMATION: AMPR
  NAME/KEY: gene
LOCATION: (647)..(1306)
OTHER INFORMATION: CMR
  OTHER INFORMATION: ori
   FEATURE:
NAME/KEY: gene
   NAME/KEY: gene
  MAME/KEY: gene
   SEQ ID NO 20
LENGTH: 6464
   FEATURE:
   FEATURE:
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APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.

Sequence 581, Application US/09887576 Patent No. US20020144047A1 GENERAL INFORMATION: APPLICANT: BudWorth, P.

US-09-887-576-581/c

RESULT 31

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Pred. No. 0.98;
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  DB 12;
  APPLICANT: Microbiological Research Authority
APPLICANT: Microbiological Research Authority
APPLICANT: The Speywood Laboratory Limited
TITLE OF INVENTION Recombinant Toxin Fragments
TILLE OF INVENTION Recombinant Toxin Fragments
CURRENT APPLICATION NUMBER: US/10/241,596
CURRENT FILING DATE: 1090-09-12
PRIOR FILING DATE: 1999-02-23
PRIOR APPLICATION NUMBER: US 09/255,829
PRIOR APPLICATION NUMBER: PCT/GB97/02273
PRIOR APPLICATION NUMBER: PCT/GB97/02273
PRIOR PILING DATE: 1997-08-22
PRIOR PLILING DATE: 1997-08-22
PRIOR PLILING DATE: 1997-12-27
PRIOR APPLICATION NUMBER: US 08/782,893
PRIOR APPLICATION NUMBER: US 08/782,893
PRIOR APPLICATION NUMBER: US 08/782,893
PRIOR APPLICATION NUMBER: GB 9625996.5
PRIOR PILING DATE: 1996-12-13
PRIOR PRILING DATE: 1996-12-13
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PRIOR PILING DATE: 1996-12-13
PRIOR PILING DATE: 1996-12-13
   Score 23.4; Di
Pred. No. 1.2;
   0; Mismatches
     CURRENT APPLICATION NUMBER: US/10/023,208
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 60/256,163
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.1
SEQ ID NO 63
  1666 GricaGCrirringracaactign 1642
  CTTGTACAACTTGT 25
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  Sequence 137, Application US/10241596 Publication No. US20030166238A1 GENERAL INFORMATION:
   Sequence 20, Application US/10151690; Publication No. US20030124555A1; GENERAL INFORMATION:
   ORGANISM: Clostridium botulinum
   NUMBER OF SEQ ID NOS: 175
SOFTWARE: PatentIn version 3.1
SEQ ID NO 137
   Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative
  93.6%;
  APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
APPLICANT: LI, XIAO
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: BYRD, DEVON R.N.
   TYPE: DNA ORGANISM: Artificial sequence
  ; OTHER INFORMATION: synthetic US-10-023-208-63
  Query Match 93.63
Best Local Similarity 96.03
Matches 24; Conservative
   US-10-241-596-137/c
  RESULT 30
US-10-151-690-20/c
  US-10-241-596-137
  TYPE: DNA
   à
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   g
  APPLICANT: BRASCH, MICHAEL A.
APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
APPLICANT: CHEO, DAVID
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: BYED, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOL
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOL
CURRENT FILING DATE: 2002-05-21
FRIOR PAPLICATION NUMBER: US 60/291,973
FRIOR PELLORICATION NUMBER: US 60/291,973
FRIOR PELLORICATION NUMBER: US 60/291,973
FRIOR PILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SSEQ ID NO 19
LENGTH: 120
APPLICANT: Byrd, Devon R.N.

TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in TITLE OF INVENTION: Recombinational Cloning
TITLE OF INVENTION: Recombinational Cloning
FILE REFERENCE: 0942.5010002
CURRENT FILING DATE: 2000-12-11
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 60/169,983
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 140
SOFTWARE: Patentin version 3.0
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  Sequence 63, Application US/10023208
Publication No. US20030124537A1
GENERAL INFORMATION:
APPLICANT: Liu, Min
APPLICANT: Liu, Yuan-Ching
TITLE OF INVENTION: PROCARYOTIC LIBRARIES AND USES
FILE REFERENCE: A-70174-1/RFT/RMS/RMK
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  TCTTGTACAACTIGT 25
  29 Gricagciririridiacaaacrici 5
  ; Sequence 19, Application US/10151690 ; Publication No. US20030124555A1
   ; OTHER INFORMATION: plasmid pDEST1
US-10-151-690-19
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ORGANISM: Artificial sequence
   TYPE: DNA ORGANISM: attR1 PCR Primer
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  US-10-151-690-19/c
   US-09-732-914-44
  FEATURE:
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```
PUBLICATION NO. US20030124555A1

GENERAL INFORMATION:

APPLICANT: BRASCH, MICHAEL A.

APPLICANT: CHEO, DAVID

APPLICANT: LI, XIAO

APPLICANT: ESPOSITO, DOMINIC

APPLICANT: ESPOSITO, DOMINIC

APPLICANT: ESPOSITO, DOMINIC

APPLICANT: ESPOSITO, DOMINIC

APPLICANT: BYRD, BYRD, BLOON R.N.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO

TITLE OF INVENTION: 0942-5122001

FILE REFERENCE: 0942-5122001

CURRENT APPLICATION NUMBER: US 10/151,690

PRIOR FILING DATE: 2002-05-21

PRIOR FILING DATE: 2001-05-21

PRIOR FILING DATE: 2001-05-21

NUMBER OF SEQ ID NOS: 64

SOFTWARE: PALENTIN VERSION 3.1

SEQ ID NO 32

LENGTH: 25
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   Gaps
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  Score 23.4; DB 14; Length 25; Pred. No. 0.47; 0; Mismatches 1; Indels C
  Length 35;
  Indels
  APPLICANT: Sherman, Amir APPLICANT: Trucheart, Joshua APPLICANT: Trucheart, Joshua APPLICANT: Trucheart, Joshua Trucheart Milne, G. TOSHUATOR MOLECULES TITE OF INVENTION: LOVE VARIANT REGULATOR MOLECULES FILE REFERENCE: 14184-009001
CURRENT PILING DATE: 2002-12-30
NUMBER OF SEQ ID NOS: 92
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 33
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Matches 24; Conservative 0; Mismatches 1;
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   1 GTTCAGCTTTCTTGTACAACTTGT 25
   1 GrichGerriririgiackakerrer 25
  35 GIICAGCITITITIGIACAACTIGI
  US-09-974-760B-33/c; Sequence 33, Application US/09974760B; publication No. US20030143705A1
   US-09-732-914-44/c
; Sequence 44, Application US/09732914
; Sequence No. US20020007051A1
; GENERAL INFORMATION:
; APPLICANT: Cheo, David
  Cheo, David
Brasch, Michael A.
Temple, Gary F.
Hartley, James L.
   TYPE: DNA ORGANISM: Artificial Sequence FEATURE:
   Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative
  APPLICANT: Roberts, Shannon
   ; OTHER INFORMATION: primer US-09-974-760B-33
  GENERAL INFORMATION:
   ; TYPE: DNA
; ORGANISM: attRl
US-10-151-690-32
   APPLICANT:
APPLICANT:
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  Gaps
   Gaps
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   ö
  Score 23.4; DB 14; Length 25; Pred. No. 0.47; 0; Mismatches 1; Indels
  93.6%; Score 23.4; DB 14; Length 25; 96.0%; Pred No. 0.47;
   Indels
   APPLICANT: Perkins, buwall
APPLICANT: length and indeabaum, Michael
APPLICANT: lindeabaum, Michael
APPLICANT: length, Josephine
APPLICANT: Fleming, Josephine
APPLICANT: Fleming, Elena
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 24601-420
CURRENT FILING DATE: 2002-05-30
CURRENT FILING DATE: 2001-05-30
PRIOR PELICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 49
LENGTH: 25
   0; Mismatches
              APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/05,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/466,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INCREMENTION:
  TOPOLOGY: both
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-162-879-9
   1 Gricagciririrgiacaaacirgi 25
  1 GITCAGCITICITGIACAACTIGI 25
  1 Gricagcitirriciacaaactici 25
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US-10-151-690-32
; Sequence 32, Application US/10151690
   Sequence 49, Application US/10161403
Publication No. US20030119104A1
GENERAL INFORMATION:
  TELEPHONE: 202-371-2600
  TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
   LENGTH: 25 base pairs
   Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative C
  TYPE: DNA
ORGANISM: Artificial Sequence
  TYPE: nucleic acid
STRANDEDNESS: both
   Query Match
Best Local Similarity 96.03
Matches 24; Conservative
   APPLICANT: Perkins, Edward
  CTHER INFORMATION: attR1
JS-10-161-403-49
   RESULT 23
US-10-161-403-49
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APPLICANT:

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CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600
   CURLET: COST

ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: BATEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/162,879
FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
   Length
  Indels
   COMPUTER: IBM PC_Compatible
OPERATING SYSTEM: PC_DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DAIR:
APPLICATION NUMBER: US/10/058,292
  Score 23.4; DB 14;
Pred. No. 0.47;
  ä
  Recombination Sites
  APPLICATION NUMBER: US/09/432,085
   0; Mismatches
  APPLICATION UNMBER: 09/432,085
FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-199
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/63,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 202-371-2600
   TOPOLOGY: Docth

MOLECULE TYPE: CDNA,

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-058-292-9
  1 GITCAGCTITCITGIACAACTIGI 25
   1 GrickGcrirrirgiackakcrigr 25
  FILING DATE: 30-Jan-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
              ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  LENGTH: 25 base pairs
   INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
   93.6%;
96.0%;
   TYPE: nucleic acid
STRANDEDNESS: both
   NUMBER OF SEQUENCES: 35
   CITY: Washington
   Query Match
Best Local Similarity 96.0
Matches 24; Conservative
  COUNTRY: USA
  US-10-162-879-9
   g
  Sequence 4, Application US/10055001A
Sequence 4, Application US/10055001A
Sequence 4, Application Would US20030049835A1
GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE OF INVENTION: using recombinational cloning
FILE REFERENCE: HELLGA and ecombinational cloning
FILE REFERENCE: HELLGA and wears 100/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOGTWARE: PatentIn version 3.1
ILENGTH: 25
ILENGTH: 25
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   Gaps
   Gaps
  APPLICANT: Hartley, James L.
Sraphicant: Hartley, James L.
Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
Recombination Sites
  ; OTHER INFORMATION: Description of Unknown Organism: recombination; CTHER INFORMATION: products
US-10-300-892-9
   .
0
  NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
  o;
  Length 25;
   Length 25;
  j OTHER INFORMATION: core sequence of recombination site attR1
US-10-055-001A-4
   Indels
  Indels
  Query Match 93.6%; Score 23.4; DB 14; Best Local Similarity 96.0%; Pred. No. 0.47; Matches 24; Conservative 0; Mismatches 1;
  Query Match 93.6%; Score 23.4; DB 12; Best Local Similarity 96.0%; Pred. No. 0.47; Matches 24; Conservative 0; Mismatches 1;
CURRENT APPLICATION NUMBER: US/10/300,892
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/907,719
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOUTWARE: Patentin Ver: 2.0
LENGTH: 25
  25
  Gricagcritrirgracaaacrigr 25
  1 GIICAGCIIICIIGIACAAACIIGI 25
   1 Gricagcrirrirgiacaaacrigr 25
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  Sequence 9, Application US/10058292
Publication No. US20030054552A1
GENERAL INFORMATION:
   TYPE: DNA ORGANISM: Artificial sequence
  TYPE: DNA
ORGANISM: Unknown
FEATURE:
   US-10-055-001A-4
  US-10-058-292-9
   FEATURE:
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Gaps

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Sequence 9, Application US/09985448

Publication No. US20030157716A1

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: APPLICANTION Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
PRIOR FILING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LEAST TEMPLE PATENTING NOTE: 2.0
SEQ ID NO 9
   Sequence 9, Application US/10300892;
Publication No. US20030175970A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Fext, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having;
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
  Gaps
   FEATURE: OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
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  ..
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  Length 25;
  Indels
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   Query Match 93.6%; Score 23.4; DB 12; Best Local Similarity 96.0%; Pred. No. 0.47; Matches 24; Conservative 0; Mismatches 1;
   Score 23.4; DB 11;
Pred. No. 0.47;
  ij
  Query Match
93.6%; Score 23.4; Di
Best Local Similarity 96.0%; Pred. No. 0.47
Matches 24; Conservative 0; Mismatches
  1 GTTCAGCTTTCTTGTACAACTTGT 25
  GTICAGCTITITIGIACAAACTIGI 25
   1 GITCAGCITICITGIACAACTIGI 25
   25
FILING DATE: 07-JUN-LL-CLASSIFICATION:
TELECOMMUNICATION: 1NFORMATION: 202-371-260
  TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
   TYPE: nucleic acid
STRANDEDNESS: both
   TOPOLOGY: both
MOLECULE TYPE: CDNA
  ORGANISM: Unknown
   RESULT 19
US-10-300-892-9
  US-09-985-448-9
   RESULT 18
US-09-985-448-9
  US-09-432-085-9
  TYPE: DNA
   à
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                                       GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Harsely, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/09/907,719
CURRENT FILING DATE: 1999-10-23
PRIOR FILING DATE: 1999-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN VET. 2.0
  Gaps
  FEATURE:
7 OTHER INFORMATION: Description of Unknown Organism: recombination
7 OTHER INFORMATION: products
US-09-907-719-9
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  Sequence 9, Application US/09432085
; Sequence 9, Application US/09432085
; Publication No. US20030100110A1
; GENERAL INFORMATION:
    APPLICANT: Brasch, Michael A.
    TITLE OF INVENTION: Recombination Sites
    NUMBER OF SEQUENCES: 35
    CORRESPONDENCE ADDRESS:
    ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
    STREET: IllO New York Ave., N. W. Suite 600
    CITY: Washington
  25;
   Length
  Indels
  STATE: DC
COUNTRY: USA
ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
CORPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
FILING DATE: (Herewith)
   Score 23.4; DB 10;
Pred. No. 0.47;
0; Mismatches 1;
   1 dricadciririrdiacaaaciidr 25
   1 GTTCAGCTTTCTTGTACAACTTGT 25
  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
  CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
   08/663,002
  08/486,139
   Query Match 93.6%;
Best Local Similarity 96.0%;
Matches 24; Conservative (
  FILING DATE: 07-JUN-1996
CLASSIFICATION:
                              Publication No. US20020192819A1
   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
  RIOR APPLICATION DATA:
APPLICATION NUMBER:
  CLASSIFICATION:
   TYPE: DNA
ORGANISM: Unknown
   RESULT 17
US-09-432-085-9
   SEQ ID NO 9
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Gaps

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Sequence 9, Application US/09907900

Sequence 9, Application US/09907900

Patent No. US20020172997al

GENERAL INFORMATION:

APPLICANT: Hartley, James L.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Temple, Gary F.

APPLICANT: Peochinational Cloning Using Nucleic Acids Having

TITLE OF INVENTION: Recombination Sites

TITLE OF INVENTION: Recombination Sites

TITLE OF INVENTION NUMBER: US/09/907,900

CURRENT FILING DATE: 2001-07-19

FRIOR APPLICATION NUMBER: 09/177,387

PRIOR APPLICATION NUMBER: 09/177,387

PRIOR APPLICATION NUMBER: 09/177,387

SOFTWARE: PatentIN Ver. 2.0

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 9

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   ; OTHER INFORMATION: Description of Unknown Organism: recombination; OTHER INFORMATION: products
US-09-907-900-9
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  ;
0
   Length 25;
  25;
   Length
   GENERAL INFORMATION:
APPLICANT: Vile, Richard G.
APPLICANT: Harrington, Kevin
APPLICANT: Bateman, Andrew
APPLICANT: Bateman, Andrew
APPLICANT: Bateman, Andrew
APPLICANT: Bateman, Andrew
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TISSUE
TITLE OF INVENTION: SPECIFIC GENE REGULATION THERAPY
FILE REFERENCE: 07039-289001
CURRENT APPLICATION NUMBER: US/09/822,634
CURRENT APPLICATION NUMBER: 6/193,977
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 18
SOFTHARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 25
   ; OTHER INFORMATION: Synthetically generated vector sequence US-09-822-634-7
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Pred. No. 0.47;
0; Mismatches 1;
   Query Match 93.6%; Score 23.4; DB 10; Best Local Similarity 96.0%; Pred. No. 0.47; Matches 24; Conservative 0; Mismatches 1;
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   1 GTTCAGCTTTCTTGTACAACTIGT 25
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US-09-907-719-9
; Sequence 9, Application US/09907719
          Sequence 7, Application US/09822634
Patent No. US20020150556A1
   93.6%; inity 96.0%; Conservative 0,
   ORGANISM: Artificial Sequence
  Query Match
Best Local Similarity
Matches 24; Conserva
   1 GTTCAGCTI
   TYPE: DNA
ORGANISM: Unknown
FEATURE:
   RESULT 15
US-09-907-900-9
   TYPE: DNA
   ВÞ
  g
   à
   APPLICANT: Cheo, David
APPLICANT: Cheo, David
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, James L.
APPLICANT: Byrd, Devon R.N.
TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in
TITLE OF INVENTION: Recombinational Cloning
FILE REFERENCE: 0942.5010002
GURRENT FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-12-11
PRIOR FILING DATE: 2000-03-09
SPRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 140
SEQ ID NO 8
LENGTHALE.
SEQ ID NO 8
LENGTH: 25
  ;
0
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   GENERAL INCOMMATION:
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION Recombination Sites
FILE REPERENCE: 1094-1265008
CURRENT FILING DATE: 2001-05-16
PRIOR APPLICATION NUMBER: 09/296,281
PRIOR APPLICATION NUMBER: 09/296,281
PRIOR APPLICATION NUMBER: 1997-04-22
PRIOR APPLICATION NUMBER: 1997-04-22
PRIOR FILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-04-22
SRIOR FILING DATE: 1997-04-22
SRIOR FILING DATE: 1997-04-22
SRIOR FILING DATE: 1997-04-22
SRIOR FILING DATE: 1997-04-22
SROFTWARE: PATENTIN VET. 2.0
SEQ ID NO 9-
   Gaps
   Gaps
   OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
   ö
   ;
0
  Length 25;
  93.6%; Score 23.4; DB 9; Length 25; 96.0%; Pred. No. 0.47; ive 0; Mismatches 1; Indels
   1; Indels
  Score 23.4; DB 9;
Pred. No. 0.47;
   0; Mismatches
   1 GTTCAGCTTTCTTGTACAACTTGT 25
   Gricageritiritigiacaaaciigi 25
   1 GIICAGCIIICIIGIACAACTIGI 25
  Sequence 9, Application US/09855797A Patent No. US20020094574A1
Sequence 8, Application US/09732914
Patent No. US20020007051A1
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96.0%;
  24; Conservative
   24; Conservative
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Best Local Similarity
Matches 24; Conserv
   Best Local Similarity
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US-09-732-914-8
   US-09-855-797A-9
   RESULT 13
US-09-855-797A-9
  Query Match
   TYPE: DNA
  Matches
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RESULT 14

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Perkins, Edward
  GENERAL INFORMATION:
   US-09-732-914-45/c
  US-09-732-914-45
  TYPE: DNA
                      APPLICANT:
APPLICANT:
  ð
  g
  à
   ő
  ,
0
   Gaps
  Gaps
   APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
Brasch, Michael A.
ITTLE OF INVENTION: Recombination Sites
   ö
  ;
0
  CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: STERNE, KESSLER, GOLDSTEIN & F.L.L.C.
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
  CUNTRY: UGA

STATE: DC

COUNTRY: UGA

ZIP: 2006-3934

COMPUTER READABLE FORM:

MEDIUM TYBE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/10/162,879

FILING DATE: 06-Jun-2002

CLASSIPICATION NUMBER: US/09/432,085

FILING DATE: 07-JNN-1999

APPLICATION NUMBER: US/09/33,493

FILING DATE: 20-JNN-1999

APPLICATION NUMBER: 09/663,002

FILING DATE: 12-JNN-1999

APPLICATION NUMBER: 08/466,139

FILING DATE: 07-UNN-1995

FILING DATE: 07-UNN-1995

TELERAX: 202-371-2640

INFORMATION POR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

SEQUENCE CHARACTERISTICS:

LENGTH: 25 base pairs

   Query Match
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 25; Conservative 0; Mismatches 0; Indels
    100.0%; Score 25; DB 14; Length 25; 100.0%; Pred. No. 0.089;
  0; Indels
  0; Mismatches
   MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-162-879-10
   1 GITCAGCITICITGIACAAACTIGT 25
  1 GIICAGCITICTIGIACAAACTIGI 25
   1 Gricascrircirstachakcrist 25
  Sequence 10, Application US/10162879
Publication No. US20030068799A1
  NUMBER OF SEQUENCES: 35
          Query Match
Best Local Similarity 100.0
Matches 25; Conservative
  GENERAL INFORMATION:
  US-10-162-879-10
  П
   à
   qq
```

```
GENERAL INFORMATION:
APPLICANT: Chee, David
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Byrd, Devon R.N.
TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in TITLE OF INVENTION: Recombinational Cloning
FILE REFERENCE: 0942.5010002
CURRENT APPLICATION NUMBER: US 60/169,983
FILE REFERENCE: 1999-12-10
FRIOR APPLICATION NUMBER: US 60/169,983
FRIOR APPLICATION NUMBER: US 60/169,00
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  Gaps
  Gaps
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  ;
   100.0%; Score 25; DB 14; Length 25; 100.0%; Pred. No. 0.089; tive 0; Mismatches 0; Indels
   Query Match
Best Local Similarity 100.0%; Pred. No. 0.098;
Matches 25; Conservative 0; Mismatches 0; Indels
   APPLICANT Greene, Any
APPLICANT Eleung, JOSEphine
APPLICANT Fleming, Elena
APPLICANT Stewart, Sandra
APPLICANT Stewart, Sandra
APPLICANT Shellard, Joan
TILL OF INVENTION CHROMOSOME-BASED PLATFORMS
FILE BEFRERNCE: 24601-420
CURRENT APPLICATION NUMBER: 05/294,758
PRIOR PILING DATE: 2002-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-30
PRIOR FILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-05-31
SOFTWARE: FASESEQ for Windows Version 4.0
SEQ ID NO 50
   1 GTTCAGCTTTCTTGTACAACTTGT 25
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  1 GIICAGCIIICIIGIACAACTIGI 25
   ; Sequence 45, Application US/09732914
; Patent No. US20020007051A1
Perez, Carl
Lindenbaum, Michael
  TYPE: DNA
ORGANISM: Artificial Sequence
  ORGANISM: attR2 PCR Primer
   Query Match
Best Local Similarity 100.0
Warches 25; Conservative
  OTHER INFORMATION: attR2 US-10-161-403-50
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RESULT 12 US-09-732-914-8

Sequence 50, Application US/10161403 Publication No. US20030119104A1 GENERAL INFORMATION:

RESULT 10 US-10-161-403-50 .

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TYPE: DNA ORGANISM: Artificial sequence
   COUNTRY: USA
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US-10-058-292-10
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  Sequence 5, Application US/10055001A
Publication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
   ô
   ö
   MESULT 0

19.10-300-892-10

19.5 Sequence 10, Application US/10300892

2 Publication No. US20030175970A1

2 GENERAL INFORMATION:

3 APPLICANT: Hartley, James L.

3 APPLICANT: Femple, Gary F.

3 APPLICANT: Femple, Gary F.

3 APPLICANT: Fox, Donna K.

3 TITLE OF INVENTION: Recombination Sites

5 TITLE OF INVENTION: Recombination Sites

5 TITLE OF INVENTION: NECOMBINATION Sites

5 TITLE OF INVENTION: NECOMBINATION Sites

6 TILE REPERENCE: 0942-2850004

7 CURRENT PILING DATE: 2001-07-11-21

7 PRIOR PILING DATE: 2001-07-19

7 PRIOR FILING DATE: 105/09/177,387

7 PRIOR PILING DATE: 105/09/177,387
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  CTHER INFORMATION: Description of Unknown Organism: recombination; CTHER INFORMATION: products
US-10-300-892-10
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OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
US-09-985-448-10
   .
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   100.0%; Score 25; DB 12; Length 25; 100.0%; Pred. No. 0.089; cive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.089;
tive 0; Mismatches 0; Indels
CURRENT APPLICATION NUMBER: US/09/985,448
CURRENT FILING DATE: 2001-11-02
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: 25
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  1 GTTCAGCTTTCTTGTACAACTTGT 25
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  25; Conservative
  Query Match
Best Local Similarity
Matches 25; Conservat
   Query Match
Best Local Similarity
Matches 25; Conserv
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ORGANISM: Unknown
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ORGANISM: Unknown
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US-10-055-001A-5
  SEQ ID NO 10
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Gaps
   APPLICANT: Hartley, James L.
Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
Recombination Sites
  ..
  NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
   FEATURE:
; OTHER INFORMATION: core sequence of recombination site attR2
US-10-055-001A-5
   Length 25;
   Query Match
Best Local Similarity 100.0%; Pred. No. 0.089;
Matches 25; Conservative 0; Mismatches 0; Indels
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COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MSG-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION MARBRE: US/10/058,292
FILING DATE: 30-Jan-2002
CLASSIFICATION: <UNknown>
using recombinational cloning
  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/432,085
FILING DATE: 1999-11-02
FILING DATE: 20-JAN-1999
FILING DATE: 20-JAN-1999
FILING DATE: 1-JAN-1998
FILING DATE: 1-JAN-1998
FILING DATE: 07-JAN-1998
APPLICATION NUMBER: 08/63,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
  TOPOLOGY: DOLD

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-058-292-10
     TITLE OF INVENTION: using recombinational FILE REFERENCE: HELICAA CURRENT APPLICATION NUMBER: US/10/055,001A CURRENT FILING DATE: 2002-06-11 NUMBER OF SEQ ID NOS: 26 SOFTWARE: Patentin version 3.1 SEQ ID NO 5 LENGTH: 25
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  ; Sequence 10, Application US/10058292; Publication No. US20030054552A1
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
  TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
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   Sequence 10, Application US/09907719; Sequence 10, Application No. US20020192819A1; Publication No. US20020192819A1; GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Pox, Donna K.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having; TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/09/907,719
CURRENT APPLICATION NUMBER: US/09/177,387
PRIOR APPLICATION NUMBER: US/09/177,387
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
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OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
US-09-907-900-10
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Sequence 10, Application Us/09412085

Publication No. 92003010011001

GREENLINGWARTON: Becombination Sites

PUBLICATION FOR INVESTION: Recombination Sites

CORRESPONDESSE: STEER, RECOMBINATION: Recombination Sites

NUMBERS OF SEGUENCE ADDRESS: A COLDSTEIN & FOX, P.L.L.C

STREET: 1100 New York Rev., N. W. Suite 600.

STREET: 1100 New York Rev., N. W. Suite 600.

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STREET: 1100 New York Rev., N. W. Suite 600.

SCHUTER READABLE OFFICE

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COMPUTER RESERVED OFFI COLORIS STREET: ADDRESS: DETERMINE ```

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RESULT 4 US-09-432-085-10

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November 6, 2003, 23:06:49; Search time 102.25 Seconds (without alignments) 780.185 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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1 gttcagctttcttgtacaaacttgt 25
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                             IDENTITY_NUC Gapoxt 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                             Sequence:
                                                                                                                                                                                    Run on:
                                                                                                                                                                                                                                                                                                    Title:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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93.6	93.6	93.6	93.6	93.6	93.6	93.6	ന	93.6	93.6	93.6	93.6	93.6	93.6	93.6	93.6	93.6				93.6			90.4	90.4				9.68
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## ALIGNMENTS

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; Sequence 10, Application US/09855797A
; Petent No. US20020094574A1
; GENERAL INFORMATION:
    APPLICANT: Hartley, James L.
    APPLICANT: Hartley, James L.
    APPLICANT: Temple, Gary F.
    APPLICANT: Temple, Gary R.
    APPLICANT: Temple, Gary R.
    APPLICANT: Temple, Gary R.
    APPLICANT: Pox, Donna K.
    TITLE OF INVENTION: Recombination Sites
    TITLE OF INVENTION: NUMBER: 0942.2850008
; TITLE OF INVENTION: NUMBER: 09/296.281
; PRIOR APPLICATION NUMBER: 09/296.281
; PRIOR PILING DATE: 1999-04-22
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; PRIOR PILING DATE: 1997-10-24
; NUMBER: OF SEQ ID NOS: 60
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; TEMPLE OF INVENTION NUMBER: 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
FOTHER INFORMATION: products
OTHER INFORMATION: products
OS-09-885-797A-10
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Matches 25; Conservative
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us-10-055-001a-11.rge

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BASE COUNT
ORIGIN
    TITLE
JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAT 26-SEP-2002
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                                                                                     Vile, R.G., Harrington, K., Murphy, S. and Bateman, A. Compositions and methods for tissue specific gene regulation therapy
Patent: WO 0174861-A 11 11-OCT-2001;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: EP 1227147-A 14 31-JUL-2002;
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Sequence 14 from Patent BP1227147.
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                            synthetic construct
synthetic construct
artificial sequences.
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VERSION
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SOUNCE
ORGANISM
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ACCESSION
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ORIGIN
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ORIGIN
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AUTHORS
TITLE
JOURNAL
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AX491653
VERSION
KEYWORDS
SOURCE
                                                                           REFERENCE
                                                                                                                                     JOURNAL
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KEYWORDS
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Recombinational cloning using engineered recombination sites Patent: EP 1229113-A 14 07-AUG-2002; INVITROGEN CORPORATION (US) Location/Qualifiers
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88.0%; Score 22; DB 6; Length 25;
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AR124534
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AUTHORS
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JOURNAL
FEATURES
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AR163185
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AX269140
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/protein id="AAN76304.1"
/db_xref="G1:25988998"
/translation="WEKKITGYTTVDISQWHRKEHFBAFQSVAQCTYNQTVQLDITAF
LKTVKKNKHKFYPAFIHILARLÄNNAHPEFRNAMKDGBLVIMDSVHPCYTVFHEQTETF
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ANMDNFFAEVFTWGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
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/note="attR1; Gateway; Bacteriophage Lambda recombination
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Haag, V.R., Lee, D.W. and Aramayo, R.
Direct Submission
Submitted (27-AUG-2002) Biology, Texas A&M University, BSBW #415,
College Station, TX 77843-3258, USA
Location/Qualifiers
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10419. .13990
/note="his-3 right flank; his-3 target integration site"
1 3549 c 3559 g 3497 t
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note="his-3 left flank; his-3 target integration site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         his-3 integration vector pUHAM007
his-3 integration vector pUHAM007
artificial sequences; vectors.
1 (bases 1 to 13990)
Haag, J. R., Lee, D. W. and Aramayo, R.
Description of a GATEWAY Destination Vector For High-Throughput Construction of Neurospora crassa Histidine-3 (his-3)-Gene Unpublished
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                                                                                                                                   Length 13274;
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His-3 integration vector pJHAM007, complete sequence.
AF541939
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/mol_type="genomic DNA"

/mol_type="genomic DNA"

/mol_type="fenomic DNA"

/mol_type="fenomic DNA"

/mol_type="genomic DN
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Pred. No. 4.4;
0; Mismatches
                                                      3482
/mol_type="genomic DNA"
/db_xref="taxon:32630"
3271 c 3178 g 34
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Best Local Similarity 95.8%;
Matches 23; Conservative
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AF541939
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TITLE
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Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: 18 6171861-A 14 09-JAN-2001;
Location/Qualifiers
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Hartley, J. L. and Brasch, M.A.
Recombinational cloning using engineered recombination sites
Patent: 18 6270369-A. 14 0'-AUG-2001;
Location/Qualifiers
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    Length 13990;
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   DB 12;
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14;
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 Score 22.4; Dl
Pred. No. 4.3;
0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 14;
Matches 22; Conservative 0; Mismatches
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AR124534
AR124534.1 GI:14109895
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Sequence 14 from patent US 6270969.
AR163185.1 GI:16233697
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Sequence 11 from Patent WO0174861.
AX269140
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/organism="unknown"
^ 5 g
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ch 89.6%;
l Similarity 95.8%;
23; Conservative (
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PAT 24-JAN-2003
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The use of genes encoding membrane transporter pumps to stimulate the production of secondary metabolites in biological cells Patent: WO 0208388-A 9 24-OCT-2002, Vlaams Interuniversitair Institutut voor Biotechnologie vzw. (BE) Location/Qualifiers
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Syngenta Participations AG (CH) ; Universitaet Zuerich (CH)
Location/Qualifiers
1. .13274
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                     4789. .5246
/note="8V40"
/gene="w"
/note="mini-white; derived from Drosophila"
/oraplement(<9370. .9819)
/transposon="piggyBac transposable element"
a 2924 c 2833 g 3497 t
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Pred. No. 4.4;
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/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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95.8%; Pred. No. 4.4;
ive 0; Mismatches
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Sequence 9 from Patent W002083888.
AX590202
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AX356862
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3326 c 3397 g 3
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Best Local Similarity 95.8%;
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Matches 23; Conservative
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priggyBac transformation vector pB-UGIR w+
prifficial sequences; vectors.
1 (bases 1 to 1267)
Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, E.P.
A toolkit for transformation and mutagenesis in Drosophila using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spana, E.P.
                                                                                  632. .998
/note="5x UAS hsp70 TATA signal"
1003. .2713
/note="Gateway recombination cassette A; attR1 CmR ccdB
                                                                                                                                                                                                           complement(3076. .4788)
/note="Gateway recombination cassette B; attR1 CmR ccdB
attR2"
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/note="Gateway recombination cassette A; attRl CmR ccdB
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/note="Gateway recombination cassette B; attRl CmR ccdB
/organism="piggyBac transformation vector pB-UGIR w+"
/mol_type="genomic DNA"
/db xref="taxon:221642"
/complement(11. .>620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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2 (Dases 1 to 12677)
2 (Dases 1 to 12677)
Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spaniert Submission
Direct Submission
Biotechnology, Inc., 3054 Cornwallis Rd, Research Tringle 27709, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .12677
/organism="piggyBac transformation vector pB-UGIR
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 12677;
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0
                                                                                                                                                                                                                                                                             /note=18740"
5247. 9369
/gene=1w"
/note="win1-white; derived from Drosophila"
complement(<9370. 9819)
/transposon="piggyBac transposable element"
a 2924 c 2833 g 3497 t
                                                                      element"
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                                                                  transposon="piggyBac transposable"
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PiggyBac transformation vector pB-UGIR w+,
AX196825
AX196825.1 GI:28565731
                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 22.4; DB 12;
Pred. No. 4.4;
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/note="5x UAS hsp70 TATA signal"
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/db_xref="taxon:221642"
complement(11..>620)
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                                                                                                                                                                                    note="RpS5"
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1 Similarity 95.8%;
23; Conservative
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/note="RpS5"
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Best Local Similarity
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AY196825/c
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ACCESSION
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circular SYN 26-FEB-2003 complete sequence.
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Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, E.P.
Direct Submission
Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, NC 27709, USA
                                                                                     artificial sequences; vectors.

1 (bases 1 to 11005)
Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, B.P.
A toolkit for transformation and mutagenesis in Drosophila using
                                                                                                                                                                                                                                          Stam, L.F. and Spana, E.P.
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piggyBac transformation vector pB-UGIR w+
artificial sequences; vectors.
1 (bases 1 to 12677)
Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, E.P.
A toolkit for transformation and mutagenesis in Drosophila using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1003. .2713 - /note="Gateway recombination cassette A; attR1 CmR ccdB attR2"
                                                                                                                                                                                                                                                                                                                                                                              /organism="piggyBac transformation vector pB-UGateway /mol type="genomic DNA" /mol traxon:221641" /db xref="taxon:221641" complement(11. .>620)
                                                                                                                                                                                                                                                                          Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle
27709, USA
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complement(<7698. .8147)
//ransposon="piggyBac transposable element"
//ransposon="piggyBac transposable element"
2528 c 2491 g 3034 t
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pB-UGateway
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PiggyBac transformation vector pB-UGIR w+,
AY196825
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Griswold, C.M., Roebuck, J., Andersen, R.O.,
Direct Submission
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Pred. No. 4.5;
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/note="5x UAS hsp70 TATA signal"
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                                                 piggyBac transformation vector
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1. .12677
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            GI:28565716
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note="RpS5"
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/note="SV40"
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AY196825
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LKTVKKNICHEYYDAFIHILARLAMBHPBFRNAMKOGELVIMDSVHPCYTVFHEQTETF
SSLWSEYHDDFRQFLHIYSQDVACYGENLAYPPKGFIENMFFVSANPWVSFTSFDLNV
ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
                                                                                                                         1263. .1568
| gene="code"
| note="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
                                                                                                                                                                                                                                              /protein id="AAM62301.1"
| Maxere="G1:215527318"
| franslation="WOFKVYTYRESRYRLFVDVQSDIIDTPGRRMVIPLASARLLSD
KVSRELYPVVHIGDESWRMMTTDMASVPVSVIGEEVADLSHRENDIKMAINLMFWGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /protein_id="AAM62303.1"
/db_xref="GI:21552740"
/translation="WQFKVYTYKRESRYRLFVDVQSDIIDTPGRRMVIPLASARLLSD
KVSRELYPV7HIGDESWRMMTTDMASVPVSVIGREVADLSHRENDIKNAINLMFWGI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     orientation of Gateway conversion containing attR1-R2 repeats, CMR gene and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="encodes a cytotoxic protein that is a potent poison of DNA gyrase" (codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation="Mekklingytyvdisqwhkkehfbafqsvaqctvnqyvqdditaf
lktvkknkhkfypafihilarlmnahpbfrnamkdgelvimdsvhpcytyfhegtet
Ssiwseyhddfrqflhiysqdvacygenlayfprgfienmffvsanpwysfybdinv
Anmdnffafyftmgryytqgdkvlmflaiqvhhavcdgfhygrmlnelqqycdbwqgg
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                                                                                                                                                                                                                                                                                                                         1610. 1736

/note="attR2 of Gateway conversion cassette frame A"
1762. 2048

/note="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"

/note="antisense orientation of Gateway conversion
cassette frame A containing attR1-R2 repeats, CMR gene
complaint force A containing attR1-R2 repeats, CMR gene
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/note="attRl of Gateway conversion cassette frame
a 2150 c 2185 g 2347 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conversion cassette frame
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/function="confers resistance to antibiotic
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Pred. No. 4.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (2073. .2199)
/note="attR2 of Gateway
complement (2241. .2546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="AAM62302.1"
db_xref="GI:21552739"
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/gene="ccdB"
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                                                                                                                                                                                                                                :="CcdB"
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                                                                                                                                                                                                      codon_start=1
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/gene="ccdB"
1263. .1568
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ilarity 95.8%;
Conservative (
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Best Local Similarity
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BASE COUNT

ORIGIN

Matches

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DEFINITION ACCESSION

RESULT 30 AY196824 LOCUS

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Gaps

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/translation="MEKKITGYTTVDISQWHRKEHFBAFQSVAQCTYNQTVQLDITAF
THYVXKNKTKEYPAFHILARLWNAHPEFRNAMKJOGELVINBSVHPOCTVFHEQTETF
SSLWSEYHDDPRQFHIYSQDVACYGENLAYFPKGFLENMFFVSANPWVSFTSFDLNV
ANWDNPFAPVPTWGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELOQYCDEWQGG
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/note="sense orientation of Gateway conversion cassette
frame A containing attR1-R2 repeats, CmR gene and ccdB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="binary plant gene silencing vector for one-step
cloning of inverted sequences"
3803. 9019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                  complement (3657. .3783)
/note="attR1 of Gateway conversion cassette frame A"
a 2150 c 2185 g 2347 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 9019)
Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.
pJawohl8-RNAi a binary vector for gene silencing in plants
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/note="attR1 of Gateway conversion cassette
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/mol_type="genomic DNA"
/db_xref="taxon:176105"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  אסט שאסט שאסט אוטס אסט Binary vector pJawohl8-RNAi, complete sequence.
AF408413
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                                                                                                                                                                                                                                                                                                                                                                                                                                Score 22.4; DB Pred. No. 4.6; 0; Mismatches
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/db_xref="GI:21552737"
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Binary vector pJawohl8-RNAi
artificial sequences; vectors.
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larity 95.8%;
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Matches 23
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JOURNAL
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LKTVKKNKHKFYPAFIHILARLANAHPBFRNAMKDGELVIMDSVHPCYTVFHEGTETR
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ANMDNFFAPVFTMGKYYTQGDKVLMFLAIQVHHAVCDGFHVGRMLNBLQQYCDEWQGG
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KVSRELYPVVHIGDESWRMMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
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/note="sense orientation of Gateway conversion cassette
frame A containing attRl-R2 repeats, CmR gene and ccdB
gene"
                                                                                                                                                               /note="binary plant gene silencing vector for one-step cloning of inverted sequences" 3803. 9019
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/note="contains intron 1 of Arabidopsis thaliana WRKY
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/note="attRl of Gateway conversion cassette frame A"
262. .921
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/note="attR2 of Gateway conversion cassette frame A"
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complement(2073, 3783)

complement(2073, 3783)

complement(2073, 3783)

complement(2073, 3199)

fnote="attR2 of Gateway conversion cassette frame A complement(2073, 2199)

fnote="attR2 of Gateway conversion cassette frame A complement(2241, 2546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           function="confers resistance to antibiotic
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/function="confers resistance to antibiotic
                                                        'organism="Binary vector pJawohl8-RNAi"
mol_type="genomic DNA"
db_xref="taxon:188084"
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/db_xref="taxon:176105"
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iocation/Qualifiers
i. .9019
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/codon start=1
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/gene="ccdB"
1263. .1568
/gene="ccdB"
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Binary vector pdawohl8-RNAi

Binary vector pdawohl8-RNAi

artificial sequences; vectors.

I (bases 1 to 9019)

Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.

pdawohl8-RNAi a binary vector for gene silencing in plants

L Unpublished

L Unpublished

L Unpublished

L Unpublished

S (bases 1 to 9019)

C (bases 1 to 9019)

S Ulker,B., Lipka,V., Rademacher,T.R. and Somssich,I.E.

Direct Submission

L Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut

f.Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829, Germany
   /protein_id="CAD83082.1"
/brotein_id="CAD83082.1"
/baxef="cd1:29335745"
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DRWEPELINDA PRODTTWRPYMATTLRKLITGELLTASRQCI DWMEDVYAGFI
LRSALPAGWFIADKSGAGGRGSRGILAALGPDGKFSRIVVIYTIGSQATMDERNRQIA
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Binary vector pJawohl8-RNAi, complete sequence.
AF408413
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Patent: World 0188121-A 10 22-NOV-2001;
Devgen NV (BB)

    .5148
    organism="synthetic construct"

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Pred. No. 5;
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Sequence 10 from Patent WO0188121.
AX306327
AX306327.1 GI:17645566
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/db_xref="taxon:32630"
/note="Plasmid pGN39"
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Use of a gateway compatible vector for transient plant transfection
Unpublished
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2168. 2463
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ANMDNFFAPVFTWGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
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                                                                                                                                                          circular SYN 27-MAR-2003
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Direct Submission

Submitted (26-MAR-2003) Jakoby M.J., Salamini, MPI for Plant
Submitted (26-MAR-2003) Jakoby M.J., Salamini, MPI for Plant

Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, GERMANY

Location/Qualifiers
                                                                                                                                                                                                                       amp gene; beta lactamase; cat gene; ccdB gene; chloramphenicol acetyl transferase; control of cell death B protein. Transfection vector pBTdest Transfection vector pBTdest
   Gaps
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protein id="CAD83080.1"
'db_xref="GI:29335743"
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1690, 1995
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456. .580
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REFERENCE

FEATURES

ORIGIN

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BD131337 25 Pp DNA linear PAT 18-SEP-2002
Recombinational cloning using nucleic acids having recombination
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PD 15-JAN-2002
PP 26-OCT-1999 UP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
Location/Qualifiers
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1 Similarity 95.8%; Pred. No. 9.1;
23; Conservative 0; Mismatches 1; Indels
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Location/Qualifiers
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Procaryotic libraries and uses
Patent: WO 02066653-A 63 29-AUG-2002;
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/organism="unidentified"
/mol_type="genomic DNA"
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Recombinational cloning using nucleic acids having recombination
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                                            PAT 26-SEP-2002
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Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
Recombinational clouding using nucleic acids having recombination
Patent: JP 2002500861-A 10 15-JAN-2002;
LIFE TECHNOLOGIES INC
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PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PF 24-OCT-1998 JP 2000518069
JAMES L HARTLEY, MICHAEL BRASCH, GARY F TEMPLE, DONNA K FOX PC C12N15/09, C12O1/68, C12N15/00
CC Description of Unknown Organism: recombination products FH Key Location/Qualifiers
FT source 1...25
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Recombinational cloning using engineered recombination sites
Patent: EF 1229113-A 10 07-AUG-2002;
INVIRROGEN CORPORATION (US)
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Pred. No. 9.1;
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Sequence 10 from Patent BP1229113.
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    /organism="unidentified"

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AX498620.1 GI:23343417
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BD131336.1 GI:23226281
JP 200250G861-A/10.
unidentified
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Best Local Similarity 95.8%;
Matches 23; Conservative
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Best Local Similarity 95.8%;
Matches 23; Conservative
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Harrley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: US $270869.A 10 07-AUG-2001;
Location/Qualifiers
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Recombinational cloning using engineered recombination sites
Patent: EP 1227147-A 10 31-JUL-2002;
INVITENCEN CORPORATION (US)
Location/Qualifiers
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Pred. No. 9.1;
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Pred. No. 9.1;
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Pred. No. 9.1;
0; Mismatches
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Sequence 10 from Patent EP1227147.
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AX491649.1 GI:22324157
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/mol_type="genomic DNA"
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Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.
Ecombinational aloning using nucleic acids having recombination
Patent: JP 2002500861-A 15 15-JAN-2002;
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PR 24-OCT-1998 JP 2000518069
PR 24-OCT-1999 JUS 09/177387 PI
JAMES L HARLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09, C12Q1/66, C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source 1. 25
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Hartley, J.L. and Brasch, M.A.
Recombinational cloning using engineered recombination sites
Patent: 18 6171861.A 10 09-JAN-2001;
Location/Qualifiers
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Similarity 96.0%; Pred. No. 3;
24; Conservative 0; Mismatches
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    /organism="unidentified"

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/db_xref="taxon:32644"
/db_xref="taxon:32644"
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JP 2002500861-A/15.
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Best Local Similarity 96.0%;
Matches 24; Conservative
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Best Local Similarity 96.0
Matches 24; Conservative
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N JP 2002500861-A/43

N JP 2002500861-A/43

PD 15-JAN-2002

PP 26-OCT-1999 US 09/177387 PI

PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI

JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC

C12N15/09,C12Q1/68,C12N15/00

CC Description of Unknown Organism: recombination products FH

Location/Qualifiers

Location/Qualifiers
                                              1 (bases 1 to 25)

Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.

Recombinational cloning using nucleic acids having recombination

Patent: JP 2002500861-A 43 15-JAN-2002;

LIFE TECHNOLOGIES INC
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(bases 1 to 25)

Hartley,J.L. and Brasch,M.A.

Recombinational using engineered recombination sites

Patent: NS 6171861-A 15 09-JAN-2001;

Location/Qualifiers
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Location/Qualifiers
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Sequence 15 from patent US 6270969.
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ARI63186.1 GI:16233698
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/mol_type="genomic DNA"
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1 a 3 c 5 g 10
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Sequence 15 from patent US 6171861.
AR124535
AR124535.1 GI:14109896
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Pred. No. 3;
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Best Local Similarity 88.0%;
Matches 22; Conservative
JP 2002500861-A/43
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1 (bases 1 to 25)
Hartley, J.L. and Brasch, M.A.
Recombinational cloning using engineered recombination sites
Patent: 18 6270959-A 15 07-AUG-2001;
Location/Qualifiers
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Recombinational clouing using engineered recombination sites
Patent: BF 1227147-A 15 31-JUL-2002;
INVITROEM CORPORATION (US)
Location/Qualifiers
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Recombinational cloning using engineered recombination sites
Patent: EP 1229113-A 15 07-AUG-2002;
INVITROGEN CORPORATION (US)
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Pred. No. 3;
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Seguence 15 from Patent EP1227147.
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                                                                              1. .25
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FEATURES

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Recombinational cloning using nucleic acids having recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="pyruvate orthophosphate dikinase (pdk)"
                                                                                                                                                                                      note="neomycin phosphotransferase II (nptII)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 18691;
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. 4621 c 4607 g 4626 t
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100.0%; Pred. No. 0.22;
iive 0; Mismatches 0;
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Best Local Similarity 100.0
Matches 25; Conservative
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BD131369.1
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BD131369
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Singht of Gasign for efficient, effective and high-throughput gene silencing in plants

Plant J. 27 (6), 581-590 (2001)
                                                                                                                           circular SYN 09-JUL-2002
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pART27"
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Waterhouse,P.M.
Direct Submissory
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1443. .7792 / Organism="Agrobacterium tumefaciens" / mol type="genomic DNA" / db xref="taxon:358" / 7793. .938R
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AJ311874.1 GI:15982218
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Cloning vector PHELLSGATE
artificial sequences; vectors.
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CVE311874/c
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ACCESSION
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KEYWORDS
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AUTHORS
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Gaps

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number=2
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transl_table=11
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Best Local Similarity
Matches 25; Conserva
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gene; promoter; speC gene; spectinomycin resistance protein;
transposon Tn7.
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Construct design for efficient, effective and high-throughput gene silencing in plants
Plant J. 27 (6), 581-590 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                             circular SYN 09-JUL-2002
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pART27"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualifiers
                                                                                                                                                                                                     .
0
                                                                                                                                                 100.0%; Score 25; DB 6; Length 25; 100.0%; Pred. No. 0.49;
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    .18691
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  /organism="unidentified"
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Recombinational cloning using engineered recombination sites
Retent: EP 1229113-A 11 07-AUG-2002;
INVITROGEN CORPORATION (US)
Location/Qualifiers
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Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: EP 1227147-A 11 31-JUL-2002;
INVITROGEN CORPORATION (US)
Location/Qualifiers
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Recombinational cloning using enginee
Patent: EP 1227147-A 16 31-JUL-2002;
INVITROGEN CORPORATION (US)
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Recombinational cloning using nucleic acids having recombination
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Recombinational cloning using engineered recombination sites
Patent: EP 1229113-A 16 0-74G-2002;
INVITROBEN CORPORATION (US)
Location/Qualifiers
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Sequence 11 from Patent EP1227147.
AX491650.
AX491650.1 GI:22324158
                                                                                                                                                                                                                                                                                                                                                                                                    25 bp Sequence 8 from Patent WO0174861. AX269137.1 GI:16542057
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1 (bases 1 to 25)
Hartley, J.L. and Brasch, M.A.
Recombinational cloning using engineered recombination sites
Patent: US 270969-A 11 07-AUG-2001;
Location/Qualifiers
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Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: 18 6171861.A.16 09-JAN-2001;
Location/Qualifiers
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AUTHORS TITLE JOURNAL

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PAT 17-0CT-2001
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Compositions and methods for tissue specific gene regulation
therapy
L therapy
Patent: WO 0174861-A B 11-OCT-2001;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
Location/Qualifiers
1. 25
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Harrley, J.L. and Brasch, M.A.
Recombinational cloning using engineered recombination sites
Patent: US 6270899-A 16 07-AUG-2001;
Location/Qualifiers
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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

Run on:  November 6, 2003, 21:07:03; Search time 601 Seconds  (without alignments)  Title:  Perfect Score: 25 Sequence:  Scoring table:  Searched:  Searched:  Search time 601 Seconds  (without alignments)  1701.732 Million cell updates/sec  1701.732 Million cell updates/sec  Scoring table:  Scoring table:  Searched:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries GenEmbl:\* Database :

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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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ORS Hartley, J. L. and Brasch, M. A.

ORS Hartley, J. L. and Brasch, M. A.

B Recombinational cloning using engineered recombination sites

RNAL Patent: US 6171861-A 11 09-JAN-2001;

Location/Qualifiers DNA 25 bp 1 Sequence 11 from patent US 6171861. AR124531 AR124531.1 GI:14109892 RESULT 1
AR124531
LOCUS
DEFINITION
ACCESSION
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SOURCE
ORGANISM REFERENCE AUTHORS TITLE JOURNAL FEATURES

PAT 16-MAY-2001

linear

ALIGNMENTS

us-10-055-001a-10.rst

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/nore="The AD-wr
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Rhabditidae; Peloderinae; Caenorhabditis.

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Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Jacotot, L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Hill, D.E. and Vidal, M.

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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Fax: 617 632 5180

Fax: 617 632 5739

Email: Marc Vidal@dici.harvard.edu

Sequence tag of Gateway entry clones. The primers used were

designed on the predicted protein encoding ORF. C. elegans ORFeome

cloning project : Contact david hill@dfci.harvard.edu or

POLYÃ-No.
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
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81.6%; Score 20.4; DB 14; Length 111;

Query Match

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Conservative 0;
Best Local Similarity
Matches 21; Conserv
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7, 2003, 00:21:00 Search completed: November Job time: 1096.75 secs

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(Rabditidae; Peloderinae; Caenorhabditis.

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Braces, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORPecone version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:6219"
/sex="Hermaphrodite and male"
/tissue_trype="whole animal"
/dev_etrage="whole animal"
/dev_etrage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
CDNAs were cloned into ppc86"
                                                                                                                                                                                                                                Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Control david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
                    C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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Tel: 617 632 5180
Fax: 617 632 5739
                                                                                Nat. Genet., (2003) In press
Contact: Vidal M
Contact: Vidal M
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115,
Fax: 617 632 5180
                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
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Dana Farber Cancer Institute
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Caenorhabditis elegans
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Contact: Vidal M
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CB388456/c
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Caenorhabditis elegans
Eukaryota, Metazoa; Nematoda, Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 11)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bartin, N., Janky, N., Moore, T., Hudson, J.R., Harley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
C. elegans Ornew version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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OSTR137H4_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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Fax: 617 632 5739
Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome clothing project: Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
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Pred. No. 9.2e+02;
0; Mismatches 1; Indels 0;
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Contact: Vidal M
Marc Vidal Laboratory
Lana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
                                                                                                                                   Location/Qualifiers
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Similarity 95.5%;
21; Conservative
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Matches

ð a RESULT 35 CB401874/c

DEFINITION

ACCESSION VERSION

KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

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Unit. Genet., (2003) in green Contact: Vidal Mark Vidal Mark Vidal Mark Vidal Mark Vidal Laboratory

Mark Vidal Laboratory

Dana Farber Cancer Institute

1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA

Tel: 617 632 5139

Email: Marc Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeomedesigned on the predicted protein encoding orf. C. elegans or contact david hill@dfci.harvard.edu or
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 106)
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,C.M., Li,S., Jacotot,L., Bertin,M., Janky,N., Moore,T., Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
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CB396817 GI:30738528
EST.
                                                                                                  Caenorhabditis elegans

Bukaryota, Metazoa, Nematoda; Chromadorea, Rhabditida; Rhabditoidea; Rhabditidae, Peloderinae, Caenorhabditis.

1 (bases 1 to 104)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, M., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V. Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORPeone version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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/clone lib="AD-wrmcDNA"/
/note="Fnh AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into PRC86"

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/organism="Caenorhabditis elegans"
/orl_type="mRNA"
/strain="N2"
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/tissue_type="whole animal"
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AUTHORS
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Caenorhabditis elegans

Eukaryora, Merazoa, Nematoda; Chromadorea, Rhabditida; Rhabditoidea

Eukaryora, Metazoa, Nematoda; Chromadorea, Rhabditida; Rhabditoidea

; Rabditidae, Peloderinae; Caenorhabditis.

1 (bases 1 to 103)

S. Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFsome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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Diama Farber Cancer Institute
1 Jimay Fund Way Smith 858, BOSTON, MA 02115, USA
1 Tel: 617 632 5180
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/strain="N2"
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Contact: Vidal M
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RESULT 36 CB396275/c DEFINITION

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Contact: Vidal M
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/mol_type="mRNA"

/strain="N2"
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1. (bases 1 to 10.2)

Reboul, J., Vaglio, P., Rual, J. F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Ptacek, J., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Poucette-Stamm, L., Hill, D.B. and Vidal, M.

C. elegans ORFeone version 1.1. experimental verification of the genome annotation and resource for proteome-scale protein
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Contact: Vidal M
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Tel: 617 632 5139

Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project: Contact david_hil@dfci.harvard.edu
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OSTR213H5_1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.
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designed on the predicted protein encoding ORF. C. elegans ORFeome cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu
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/sex="Hermaphrodite and male"
/tissue_type="whole animal"
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/strain="N2"
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Eukaryotta, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea a Rhabditidae, Peloderinae, Caenorhabditis.

(bases 1 to 103)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
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OSTR169D10_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB396276
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Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
Sequence tag of Gateway entry clones. The primers used con-
seasigned on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
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/dow tatge="mixed stage"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of CDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
a 25 c 17 g 32 t
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Tel: 617 632 5180
Fax: 617 632 5739

    .103 "caenorhabditis elegans"
/organism="Caenorhabditis elegans"
/mll type="mRNA"
/strain="N2"
/db_xref="taxon:6239"

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Eukaryotta, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea Eukaryotta, Metazoa, Nematoda, Caenorhabditis.

(bases 1 to 10.2)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.K., Harley, J.L., Brasch, M.A., Vaddenhaute, J., Boulton, S., Braces, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P. Poucette-Stamm, L., Hill, D.E. and Vidal, M. Chectte-Stamm, L., Hill, D.E. and Vidal, M. Gordene, Stamm, L., Hill, D.E. and Vidal, M. Gordene annotation and resource for proteome-scale protein
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                                                                                                                                                                                                                                                                                                                                                   Email: Marc Vial@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
POLYA=No.
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genome annotation and resource for proteome-scale protein
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Exar: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
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                                                                                                         Nat. Genet., (2003) In press
Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115,
Fax: 617 632 5739
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/organism="Caenorhabditis elegans"
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Contact: Vidal M
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                                                                                           Enkaryotes, Metazoas, Nematodas, Chromadoreas, Rhabditidas, Rhabditidaes, Peloderinaes, Caenorhabditis.

(Rhabditidaes, Peloderinaes, Caenorhabditis.

(Bases 1 to 100)

Reboul, J., Vagalio, P., Rual, J. F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J. R., Hartley, J. L., Brasch, M. A., Vandenhaute, J., Boulton, S., Braces, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P. P.

Doucette-Stamm, L., Hill, D.E. and Vidal, M. C. elegans OrRecome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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1 (bases 1 to 100)

1 (chases 1 to 100)

2.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P., Pacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H., Tolias,P.P., Doucette-Stamm,L., Hill,D.E. and Vidal,M.
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc_vidal@dfci.harvard.edu
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//tissue_type="whole animal"
//dev_srage="mixed stage"
//clone_lib="Ab-wrmcDNA"
//clone_lib="Ab-wrmcDNA"
//clone="The Ab-wrmcDNA"
//clone="The Ab-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into ppc98.

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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
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/mol_type="mkNA"
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Contact: Vidal M
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(bases 1 to 100)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Braces, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeenew version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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                                                                           worms of
/clone lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A).
RNA isolated from both hermaphrodite and male N2 worms o all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"
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Pred. No. 9.1e+02;
0; Mismatches 1; Indels 0
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Nat. Genet., (2003) In press
Contact: Vidal Marc Vidal Laboratory
In ana Farber Cancer Institute
I Jimmy Fund Way Smith 858, BOSTON, MA 02115,
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/organism="Caenorhabditis elegans"
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95.5%; ]
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AUTHORS
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Matches

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/Stran="na" / Stran="na" / bb xref="taxon:6239" / sex="Hermaphrodite and male" / fissue_type="whole animal" / fissue_type="whole animal" / dev_stage="mixed stage" / clone lib="AD-wrmcDNA library was generated with poly(A) + RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The CDNAs were cloned into pPC86" | 34 a 22 c 18 g 26 t
                                                                                                                                             Caenorhabditis elegans
Caenorhabditis elegans
Caenorhabditis elegans
Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
1 (bases 1 to 100)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, J.R., Hartley, J.L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S.,
Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P.
Doucette-Stamm, L., Hill, D.E. and Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the
CB398867 100 bp mRNA linear EST 15-MAY-2003
OSTR21044_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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Fax: 617 632 5739

Email: Marco Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFcome
cloning project : Contact david_hill@dfci.harvard.edu or
POLYÃ-No.
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Contact: Vidal M
Marc Vidal Laboratory
Lana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115,

    .100
    .70ganism="Caenorhabditis elegans"
/mol type="mRNA"
/strain="N2"

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CB402581/c
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Eukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.

(Dases 1 to 97)
Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,C.M., Li,S., Jacotot,L., Bartin,N., Jarky,R., Moore,T., Hudson,J.R., Harsley,J.L., Bertin,N., Vanky,R., Moore,T., Hudson,J.R., Harsch,M.A., Vandenhaute,J., Boulton,S., Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P., Ptacek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
C. elegans Orrecewershon 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
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OSTET90AS_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB401179
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                                                                                    Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 859, BOSTON, MR 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Fmail: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact david hill@dfci.harvard.edu or
POLYĀ-No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="Hermaphorotice and male"
/tissue_type="whole animal"
/dev stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of CDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFecme
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Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Nay Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
                                                                                                                                                                                                                                                                                                                                                                                  /organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
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Matches 21; Conservative
                                           Nat. Genet., (20
Contact: Vidal M
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à 유 KEYWORDS

SOURCE

TITLE

COMMENT

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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea Rhabditidae; Peloderinae; Caenorhabditis.

1 (Basea I to 98)

1 (Chasea I to 98)

2 (Masea I to 98)

2 (M. Li,S., Jacotor,L., Bertin,N., Janky,R., Moore,T., Hudson,J.T., Hartley,J.L., Brasch,M.R., Vandenhaute,J., Boulton,S., Brack,J., Brack,M.R., Vandenhaute,J., Boulton,S., Praces,J., Snyder,M. Huang,R., Chance,M.R., Lee,H., Doucette-Stamm,L., Hill,D.E. and Vidaal,M.
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OSTF215C2_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB402581
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| Coore lib="AD-wrmcDNA"
| note="The AD-wrmcDNA library was generated with poly(A) +
| RNA isolated from both hermaphrodite and male N2 worms of
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
                                                                                                                                                                                                                                                                                                                                                                                                                        all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The CDNAs were cloned into pPC86"

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cloning project : Contact david_hill@dfci.harvard.edu or marc_vidal@dfci.harvard.edu POLYA=No.
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Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
Ijmmy Fund Way Smith 858, BOSTON, MA 02115,
Tel: 617 632 5189
Fax: 617 632 5739
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/organsm="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
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/tissue_type="whole animal"
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strain="N2"
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Caenorhabditis elegans
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/BLAKEF="Maxon:6239"
//BLAKEF="Maxon:6239"
//Sex="Hermaphrodite and male"
//tissue_type="whole animal"
//dev_stage="wixed stage"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
CDNAs were cloned into pPC86"
39 a 16 c 16 g 24 t
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Contact: Vidal M
Marc Vidal Laboratory
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Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
POLYÑ-No.
                                            Eukaryotta; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 95)

1 (bases 1 to 95)

C.M., Li,S., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong, C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Budson,J.R., Harley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S., Bracek,J., Jannas,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P.

Doucette-Stamm,L., Hill,D.E. and Vidal,M.

C. elegans ORFeene version 1.1: experimental verification of the
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OSTF198G7_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB401751
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Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea
; Rhabditidae, Peloderinae, Caenorhabditis.
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Pred. No. 9e+02;
0; Mismatches 1; Indels
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95.5%;
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Contact: Vidal Laboratory
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Dana Farber Cancer Institute
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Tel: 617 632 5180
Fax: 617 632 5180
Fax: 617 632 5739
Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding OMF. C. elegans OMFeome cloning project: Contact david_hill@dfci.harvard.edu or marc vidal@dfci.harvard.edu
POLYĀ=No.
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Rhabditidae; Peloderinae; Caenorhabditis.

Reboul, J., Vagilo, P., Rual, J. F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J. R., Hartley, J. L., Brasch, M. A., Vadenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans OrRecome version 1.1. experimental verification of the genome annotation and resource for proteome-scale protein
                                                                                                                                                                              CB402408 94 bp mRNA linear EST 15-MAY-2003
OSTIT212B6_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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OSTET19E71
CB400591.1 GI:30742318
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/clone_lib="AD-wrmcDNA"
/note="Hab AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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/strain="N2"
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81.6%; Score 20.4; DB 14;
Best Local Similarity 95.5%; Pred. No. 9e+02;
Matches 21; Conservative 0; Mismatches 1;
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/tissue_type="whole animal"
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CAGCTTTTTTGTACAAAGTTGG
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CB402408/c
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/organism="Caenorhabditis elegans"

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Pred. No. 9e+02;
0; Mismatches
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/tissue_type="whole animal"
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/strain="N2"
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ilarity 95.5%;
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Contact: Vidal M
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CB402537/c
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Caenorhabditis elegans
Bukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
Bukaryota, Metazoa; Nematoda; Chromadorea; Rhabditidae; Peloderinae; Caenorhabditis.

[ (bases 1 to 90)
Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, J.R., Lax, Jartley, J.L., Brasch, M.N., Vandenhaute, J., Boulton, S., Brdress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Pacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for protecome-scale protein
                                                                                                                  / blrdain: // clasue type="whole animal" // close targe="whole animal" // close lib="AD-wrmcDNA" // close lib="AD-wrmcDNA library was generated with poly (A) + RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly (A) priming. The CDNAs were closed into ppc86"
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OSTF163A10 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB392047
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Email: Marc_Vidal@dfci.harvard.edu

Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact david_hill@dfci.harvard.edu

marc_vidal@dfci.harvard.edu
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                                                       1. .87
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sex="Hermaphrodite and male"
/tissue_type="whole animal"
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/clone_lib="AD-wrmcDNA"
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Contact: Vidal M
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marc_vidal@dfci.harvard.edu
POLYA=No.
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/strain="N2"
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SOURCE
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                                    FEATURES
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Caenorhabditis elegans
Exarorhabditis elegans
Enkaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditodea
Enkaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditodea
Enkaryota, Metazoa, Nematoda, Caenorhabditis.

1 (bases 1 to 92)
Enchantion, Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bratin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Doucette-Stamm, L., Hill, D.E., May Vidal, M.
C. elegans ORFeome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Marc Vidal Laboratory
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5739
Email: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
                                                                                                                                                                                                                                                                                           CB402537 92 bp mRNA linear EST 15-MAY-2003
OSTEC14C1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB402537
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/clone lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A) +
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into PPC86"

a 26 g 28 t
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a

Matches

VERSION KEYWORDS SOURCE ORGANISM

ACCESSION

REFERENCE AUTHORS

TITLE

JOURNAL

COMMENT

CA986810/c DEFINITION

RESULT 18

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Caenorhabditis elegans
Caenorhabditis elegans
Eukaryotta; Mercazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
Eukaryotta; Mercazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

I (bases 1 to 87)
St Reboul, ", Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong, C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P.,
Doucette-Stamm,L., Hill,D.E. and Vidal,M.
C. elegans ORPeome version 1.1: experimental verification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rissue type="NECROBLASTOMA"
/cione lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pcWySPORT 6; 1st strand cDNA was primed
with a NotL-ollgo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pcMySPORT 6 vector.
Library was not normalized."

230 c 170 g 274 t 1 others
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OSTETETOB_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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Tel: 617 632 5180
Fax: 617 632 5739
Fax: 617 632 5739
Faxil: Marc_Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFecme
cloning project : Contact david_hill@dfci.harvard.edu or
                              Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Mupublished
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3874.r For
                                                                                                                                                                                                                                                                                                                                                                                                       http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOBAE002ZB04_AE00123_2&cluster=3874.r.
cgi-bin/cluster.cgi?seq=CSOBAE002ZB04_AE00123_2&cluster=3874.r.
Contact : Feng Liang Email : fliang@lffetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOBAE002ZB04_AE00123_2.
Location/Qualifiers
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Pred. No. 7.8e+02;
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/organism="Homo sapiens"
/organisms="Homo sapiens"
/ol_type="mxxxxx:3606"
/clone="CLOBB014ZD12"
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Dana Farber Cancer Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CB400039.1 GI:30741766
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Nat. Genet., (20
Contact: Vidal M
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CB400039/c
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//mol type="mmna"
//mol type="mmna"
//mol type="mmna"
//mol type="mmna"
//mose="whoro (stage 10)"
//lab host="mlning (phage-resistant)"
//lab host="mlning (phage-resistant)"
//lab host="mlning (phage-resistant)"
//lab host="mlning (phage-resistant)"
//lab host="mlning (bhage-resistant)"
//mole="wycetor: pcWr-SPORTS (site 1: Not!; Site 2: Sall;
//mole="wycetor: pcWr-SPORTS (site 1: Not!) (site 3: Sall;
//mole="wycetor: pcWr-SPORTS (site 3: Sall;
//mole="wycetor: pcWr-S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
Tissue Procurement: Martha Rebbert, Steven L. Klein, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: NGT-CGAP clone distribution information clone distribution: NGT-CGAP clone distribution information
Plate: LLAM14482 row: e column: 13
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Barrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodinae; Xenopus.

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
       Gaps
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AGENCOURT_11113724 NICHD_XGC_Emb1 Xenopus laevis cDNA clone
AMAGE:6863318 5', mRNA sequence.
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High quality sequence stop: 477.
Location/Qualifiers
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0; Mismatches
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                                                                        1 GTTCAGCTTTTTTGTACAAGTTGG
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EST.
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Conservative
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22;
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FEATURES

VERSION KEYWORDS SOURCE ORGANISM

LOCUS

ACCESSION

RESULT 19 BX430288

BASE COUNT ORIGIN

Best Loc Matches

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Gaps

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(1-2)

selected

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/dev_stagg="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
/note="Genomic DNA from strain W14 was size selected kb) and then cloned into M13 Janus."
146 c 162 g 175 t 3 others
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/mol_type="genomic DNA"
/strain="WH"
ddb_xref="taxon:29488"
/clone="PLG01864"
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Best Local 8
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1 (bases 1 to 664)

ffrench-Constant, N. H., Waterfield, N., Burland, V., Perna, N.T.,

ffrench-Constant, P. H., Waterfield, N., Burland, V., Perna, N.T.,

A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                             /notes="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
72 c 63 q 101 t 24 others
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Department of Biology and Biochemistry
Department of Biology and Biochemistry
Diversity of Bath
South Building, Bath BAZ 7AX, UK
Tel: (44) 1225 826679
Fax: (44) 1225 826779
Email: bestree@bath.ac.uk
This is one of 2,122 random reads from the MI3 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
Coli Ki2 genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                             Email: Destrobath.ac.uk

Email: Destrobath.ac.uk

This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome; please see ffrench-Constant et al. 2000, Nucleic
Acids Res.
Seq primer: M13 Forward
Class: Shotgun.
Location/Qualifiers
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Photorhabdus luminescens genomic clone PLG01864, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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Pred. No. 7.2e+02;
0; Mismatches 3; Indels 0
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Contact: ffrench-Constant RH
Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
                                                                                                                                                                                                                                                                                                           /mol_type="genomic DNA"
/strain="W14"
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/clone="PLG02205"
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AQ991011.1 GI:9649605
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hes 22; Conservative
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GSS 14-AUG-2000
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1 (bases 1 to 751)

1 (firench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.

A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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hits is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
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Rfc00126 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG00126, genomic survey
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Score 20.8; DB 28; Length 664;
Pred. No. 7.6e+02;
0; Mismatches 3; Indels 0;
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/mol_type="genomic DNA"
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/clone="PLG00126"
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
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Best Local Similarity
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/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."
163 c 174 g 204 t 5 others
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The french-Constant, R. H., Materfield, N., Burland, V., Perna, N.T.,

Daborn, P. J., Bowen, D. and Blattner, F. R.

A genomic sample sequence of the entomopathogenic bacterium

Photorhabdus luminescens W14: potential implications for virulence

20376333

10919786
                                                                                                                                                                                                                                                                                    Contract: ffrench-Constant RH
Contract: ffrench-Constant RH
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University of Bath
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Tel: (44) 1225 826621
Fax: (44) 1225 826621
Email: bssrfc@bath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Rfc02205 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG02205, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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    . 769
/organism="Photorhabdus luminescens"

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/clone="PLG01245"
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AQ991303.1 GI:9649897
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AQ990470.1
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AQ991303/c
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170 c 171 g 203 t 5 others
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Enterobacteriaceae; Photorhabdus.
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This is one of 2,122 random reads from the M13 library. For
annotation of identified clones (BLASTX, BLASTN and mapping to E.
coli K12 genome) please see ffrench-Constant et al. 2000, Nucleic
                                                                                                                                                                                                                       AQ990110 764 bp DNA linear GSS 14-AUG-Rfc00827 Photorhabdus luminescens strain W14 M13 library Photorhabdus luminescens genomic clone PLG00827, genomic survey
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Rfc01245 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01245, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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  Score 21.8; DB 28; Length 743; Pred. No. 3.1e+02; 0; Mismatches 2; Indels 0
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/mol type="genomic DNA"
/strain="W14"
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Pred. No. 3.2e+02;
0; Mismatches 2
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Department of Biology and Biochemistry
University of Bath
South Building, Bath BA2 7AX, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
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/clone="PLG00827"
                                                                                                                       626 Gricagerrirrirahachagrieg 602
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Class: shotgun.
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GSS.
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Best Local Similarity 92.0%;
Matches 23; Conservative (
Query Match
Best Local Similarity 92.0%;
Matches 23; Conservative
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AQ990470/c
LOCUS
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AQ990110/c
LOCUS
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Gaps

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GSS 14-AUG-2000

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Location/Qualifiers
1. .712
/organism="Photorhabdus luminescens"
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                                                       /mol_type="genomic DNA"
/strain="W14"
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/strain="W14"
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/clone="PLG01106"
                                                                                           /db_xref="taxon:29488"
/clone="PLG01638"
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Location/Qualifiers
1. 743
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VERSION
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PUBMED
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Daborn,P.J., Bowen,D. and Blattner,F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hote="Genomic DNA from strain W14 was size selected (1-2 ib) and then cloned into M13 Janus." 148 c 165 g 187 t 2 others
                                 Contact: ffrench-Constant RH
Department of Biology and Biochemistry
Department of Biology and Biochemistry
Department of Biology and Biochemistry
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bestreombath.ac.uk
This is one of 2,122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to B.
Coll K12 genome) please see ffrench-Constant et al. 2000, Nucleic
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Tel: (44) 1225 826621
Fax: (44) 1225 826779
Email: bssrfc@bath.ac.uk
This is one of 2.122 random reads from the M13 library. For annotation of identified clones (BLASTX, BLASTN and mapping to E.
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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Photorhabdus luminescens genomic clone PLG01638, genomic survey
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/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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Pred. No. 3.1e+02;
0; Mismatches 2; Indels 0
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/mol type="genomic DNA"
/strain="W14"
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Department of Biology and Biochemistry
University of Bath
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/clone="PLG01894"
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Seq primer: M13 Forward
Class: shotgun.
Location/Qualifiers
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AQ990809.1 GI:9649403
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AQ990809/c
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ORIGIN
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GSS 14-AUG-2000
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(Efrench-Constant, N.H., Waterfield, N., Burland, V., Perna, N.T.,
Daborn, P.J., Bowen, D. and Blattner, F.R.
A genomic sample sequence of the entomopathogenic bacterium
Photorhabdus luminescens W14: potential implications for virulence
Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
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158 c 169 g 200 t 2 others
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Department of Biology and Biochemistry
Diniversity of Bath
South Building, Bath BA2 7AY, UK
Tel: (44) 1225 826621
Fax: (44) 1225 826779
Fax: (44) 1225 826779
Faxi: (54) 1225 826
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Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
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Rfc01106 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01106, genomic survey
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/dev stage="primary phase variant"
/clone_lib="Photorhabdus luminescens strain W14 M13
library"
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/clone_lib≈"Photorhabdus luminescens strain W14 M13
library"
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Query Match

à a RESULT 8 BQ156404/c LOCUS

DEFINITION ACCESSION

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS

REFERENCE

JOURNAL

COMMENT

TITLE

FEATURES

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597 bp mRNA linear EST 16-AUG-2001 EST533345 tomato callus, TAMU Lycopersicon esculentum cDNA clone BI422679
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/tissue type="callus"
/dev stage="25-40 days old"
/lab host="XL1-Blue MRF"
/lab host="XL1-Blue MRF"
/clone lib="tomato callus, TAMU"
/note="Vector: pBlueScript SK(-1): Site_1: EcoRl; Site_2:
XR0; supplier: Glovannon! laboratory; CLEC - Cotyledons
of seellings 7-10 days post-germination were excised, cut
at both ends and placed on MS medium with no selection.
Mixed callus was harvested at 25 and 40 days and included
undifferentiated masses: Tomato Callus EST Library"
a 109 c 131 g 164 t
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                                                                                                                                                                                                                                        Lycopersicon esculentum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 597)
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Photorhabdus.
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Rfc01894 Photorhabdus luminescens strain W14 M13 library
Photorhabdus luminescens genomic clone PLG01894, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
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/clone="cleC71G2"
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/cultivar="TA496"
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Matches 23; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished
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VERSION
KEYWORDS
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AUTHORS
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/clone lib="Irradiated"
/clone lib="Irradiated"
/clone lib="Vector: Lambda 22p; Seedlings were exposed either
to lib gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. CDNA was prepared
harvested 14 hours post-treatment. CDNA was prepared
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using ExAssist
helper phage and the B. coll strain XII-Blue MRF'
(Stratagene). Excised plasmids were plated using SOLR
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Medicago truncatula
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermaryophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Pred. No. 3e+02;
0; Mismatches 2; Indels 0;
  Length 472;
                                                  Indels
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tex: 580 221 7391
Exa: 580 221 7380
Email: gdmay@noble.org
87.2%; Score 21.8; DB 13;
92.0%; Pred. No. 3e+02;
iive 0; Mismatches 2;
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Insert Length: 473 Std Error: 0.00
Plate: 092 row: E column: 03
Seq primer: TCACAGAGAAACAGCTATGAC.
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                                                                                                                                           380 GTTCAGCTTTTTTATACTAAGTTGG 356
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/db xref="taxon:3880"
                                                                                                      1 GITCAGCTITITIGIACAAAGTIGG 25
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92.0%;
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Best Local Similarity
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                             Best Local Similarity
Matches 23; Conserv
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GSS 14-AUG-2000

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Standard, J., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Nikaido, I., Osato, N., Saito, R., Suzuki, H., Yamanaka, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schonbach, C., Gojobori, T., Baldarelli, R., Hill, D. P., Bilt, C., Hune, D. A., Quackenbush, J., Schrimli, M., Kanapin, A., Batecher, C.F., Forrest, J. E. G. Cousine, S., Dalla, E., Dragani, T.A., Fletcher, C.F., Forrest, A., Frazer, K.S., Gassterland, T., Gariboldi, M., Gissi, C., Godzik, A., Gough, J., Grimmond, S., Gustincich, S., Hirokawa, N., Jackson, I.J., Jarvis, E. D., Kanai, A., Kawaji, H., Kawasawa, Y., Kedzierski, R.M., King, B. L., Konagaya, A., Kurochkin, L. Dee, Y., Lenhard, B. I., Loons, P. A., Karochkin, J., Dee, Y., Lenhard, B., Iyons, P. A., Maglott, D. R., Mallais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W.J., Pertea, G., Petrovsky, N., Pillai, R., Pontius, J. U., Qi, D., Ramachandran, S., Ravasi, T., Reed, J. C., Rend, D. J., Reid, J., Reid, J., Ramachandran, S., Ravasi, T., Wanner, L., Wahlestedt, C., Watamara, K., Shimada, K., Sullen, M., Sandelin, A., Schneider, C., Semple, C.A., Satou, M., Sakaume, N., Sato, K., Shiraki, T., Waki, K., Kawai, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashistume, W., Imotenni, K., Ishii, Y., Lich, M., Kagwa, T., Woshino, M., Wayara, D., Bhibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, A., Ahalysis of the mouse transcriptome based on functional annotation of 60,770 full-length conne
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The Institute of Physical and Chemical Research (RIXEN)
1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan Fax: 81-45-503-9216
Email: genome-resegscriken.go.jp,
RIL:http://genome-resegscriken.go.jp,
Alzawa.K., Akimura.T., Arakawa.T., Carninci,P., Fukuda,S., Hirozane,T., Inforani,K., Rimura,T., Arakawa.T., Carninci,P., Fukuda,S., Hirozane,T., Murata,M., Nakamura,M., Nomura,K., Numazaki,R., Ohno,M., Sakai,K., Sakai,W., Sakai,W., Waki,K., Watahiki,A., Muramatsu,M., and Hayashizaki,T. Tagami,M., Waki,K., Watahiki,A., Muramatsu,M. and Hayashizaki,Y. Direct Submission
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Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
RIKBN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library was grepared and sequenced in Mouse Genome CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RikEN.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Please visit our web site (http://genome.gsc.riken.go.jp) for further details.
Location/Qualifiers
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PUBMED
                                                                                     REFERENCE
                                                                                                                                    AUTHORS
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/db\_xref="taxon:10090"

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/dev_stage="seedlings"
/dev_stage="seedlings"
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/note="Vector: Lambda Zap; Seedlings were exposed either
to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared from
polyA+ enriched, pooled samples of equivalent amounts of
total RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using ExAssist
helper phage and the E. coli strain XII-Blue MRF.
(Stratagene). Excised plasmids were plated using SOLR
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosid
; eurosids I, Fabales, Fabaceae, Papilionoideae, Trifolieae,
/clone="L430040C03"
/tissue type="whole body"
/dev_stage="18 days embryo"
/clone lib="RIKEN full-length enriched, 18 days embryo
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Contact: May Go
That Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7391
                                                                                                                                                                                                 Score 21.8; DB 13;
Pred. No. 2.9e+02;
0; Mismatches 2;
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Insert Length: 472 Std Brror: 0.00
Plate: 104 row: D column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
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/db_xref="taxon:3880"
/clone="NF104D07IR"
                                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NF104D07IR 5', mRNA sequence.
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92.0%;
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BQ157398/c
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Query Match Best Local Similarity

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EST.

ORGANISM

REFERENCE AUTHORS

JOURNAL

TITLE

FEATURES

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 4 CB388073/c

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/tissue_type="seedlings"
/dev_stage="seedlings"
/dev_stage="seedlings"
/dev_stage="seedlings"
/diome_lib="irradiated"
/note="Vector: Lambda Zap; Seedlings were exposed either
/note="Vector: Lambda Zap; Seedlings were exposed either
to 100 gy gamma or 0.5, 1, 5, or 10 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared
fotal RNA from each sample. The cDNA was directionally
ligated into the Uni-Zap XR vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-Zap XR vector using Exassist
helper phage and the B. coll strain XLI-Blue MRF.
Stratagene). Excised plasmids were plated using SOLR
                                                                                                                                                                           Medicago truncatula
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids
, eurosids I, Rabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                              Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Imman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula irradiated library
Unpublished
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     EST 24-APR-2002
206 bp mRNA linear EST 24. NF092F02IR1F1027 Irradiated Medicago truncatula cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Pax: 580 221 7391
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Medicago truncatula"
|mol_type="mkmA"
|db_xref="taxon:3880"
|clore="NP692F02IR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: gdmay@noble.org
Insert_Length: 206 Std Error: 0.00
Plate: 022 row: F column: 02
Seg primer: TCACACAGGAAACAGCTATGAC.
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                                                  NF092F02IR 5', mRNA sequence.
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Mus musculus (house mouse)
Mus musculus
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92.0%;
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Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 859, BOSTON, MA 02115, USA
Tel: 617 632 5180
Fax: 617 632 5190
Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact david_hill@dfci.harvard.edu or
POLYĀ=No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENKARYOCEAN METAZOSA Nematoda; Chromadorea; Rhabditida; Rhabditoidea Rhabditidae; Peloderinae; Caenorhabditis.

(Rabbditidae) Peloderinae; Caenorhabditis.

(Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Pracek, J., Snyder, M.A., Vandenhaute, J., Boulton, S., Pracek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORPeane version 1.1: experimental verification of the genome, annotation and resource for proteome-scale protein
                                                                                                                                                                                                                                                                                       СВЗВВО73 141 bp mRNA linear EST 15-MAY-2003
OSTF091E12_1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
CB388073
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/clone_lib="AD-wrmcDNA"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
CDNAs were cloned into ppc86"
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                          Length 121;
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nol_type="mRNN"
strain="N2"
/db_xref="taxon:6239"
                       88.0%; Score 22; DB 14; L
100.0%; Pred. No. 2.2e+02;
iive 0; Mismatches 0;
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Caenorhabditis elegans
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RESULT 5 BQ156416/c

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marc_vidal@dfci.harvard.edu
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                                                                                                                                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                  /strain="N2"
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RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
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Bukaryota, Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea
; Rhabditidae; Peloderinae; Caenorhabditis.

1 (bases 1 to 108)

Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandanhaute, J., Boulton, S.,

Bndress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolias, P.P., Ptacek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H.,

Doucette-Stamm, L., Hill, D.E. and Vidal, M.

C. elegans ORFeame, version 1.1: experimental verification of the genome annotation and resource for protecome-scale protein
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SYRE212B 1 AD-wrmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
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Email: Marc Vidal@dfci.harvard.edu
Gequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david_hill@dfci.harvard.edu or
marc vidal@dfci.harvard.edu
             Email: Marc Vidal@dfci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project: Contact david_hill@dfci.harvard.edu or
marc vidal@dfci.harvard.edu
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5189
Fax: 617 632 5739
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 88.0%; Score 22; DB 14; I
1 Similarity 100.0%; Pred. No. 2.2e+02;
22; Conservative 0; Mismatches 0;
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Contact: Vidal M
617 632 5739
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Caenorhabditis elegans
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Caenorhabditis elegans
Eukaryota, Metazoa, Nematoda, Chromadorea, Rhabditida, Rhabditoidea
Eukaryota, Metazoa, Nematoda, Caenorhabditis.

(bases 1 to 121)
(bases 1 to 121)
(c.M., Li,S., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M., Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T., Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
Endress,G.A., Jenna,S., Chevet,E., Papasotiropoulos,V., Tolias,P.P., Precek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
C. elegans ORRene version 1.1: experimental verification of the genome annotation and resource for protecome-scale protein
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Contact: Vidal M
Marc Vidal Laboratory
Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
Tel: 617 632 5139
Email: Marc Vidal@fci.harvard.edu
Sequence tag of Gateway entry clones. The primers used were
designed on the predicted protein encoding ORF. C. elegans ORFeome
cloning project : Contact david hill@dfci.harvard.edu or
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OSTRO99E7_1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.
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/clone lib="AD-wrmcDNA"
/note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
CDNAs were cloned into ppc86"
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/tissue_type="whole animal"
/tissue_type="whole animal"
/dev_etage="mixed stage"
/dev_etage="mixed stage"
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/note="The Ab-wrmcDAB."
/note="The Arge of the poly (A) +
RNA isolated from both hermaphrodite and male N2 worms of
subsequent generation of cDNAs by poly (A) priming. The
CDNAs were cloned into pPC86"
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100.0%; Pred. No. 2.2e+02;
iive 0; Mismatches 0;
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/tissue_type="whole animal"
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RESULT 1
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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BO15641	BY11559	BO15739	B015640	BI42267	AQ99103	A099080	A099034	A099011	AQ99047	A099130	AQ99101	AQ98956	CA98681	BX43028	CB40003	CB39204	CB4025	CB4024	CB4005	CB4017	CB4011	CB4025	CB3920	CB3988	CB398991	CB4005	CB3920	CB3990	CB3962	CB4018	CB3962	CB3968	CB3884	CB3944	CB3955	CB3962	CB3975	CB3983	CB4020	CB3967	
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				AL Nat. Genet., (2003) In press Contact: Vidal M Marc Vidal Laboratory Dana Farber Cancer Institute 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA Tel: 617 632 5180
ESCUL B402238/c OCUS EFINITION CCESSION ERSION EYWORDS	OURCE	EFERENCE	TITLE	JOURNAL:

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TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in TITLE OF INVENTION: Recombinational Cloning
FILE REFERENCE: 0942.5010002
CURRENT APPLICATION NUMBER: US/09/732,914
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 60/169,983
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 60/189,020
PRIOR APPLICATION NUMBER: US 60/189,020
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 140
SEQ ID NO 10
LENGTHR 27
TYPE: DAA
TYPE: DAA

CORGANISM: attp2
US-09-732-914-10
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Score 23.4; DB 14; Length 25; Pred. No. 1.1; 0; Mismatches 1; Indels C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Berez, Carl
APPLICANT: Greene, Amy
APPLICANT: Greene, Amy
APPLICANT: Greene, Amy
APPLICANT: Leung, Josephine
APPLICANT: Leung, Josephine
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Sandra
TITLE OF INVENTION: CHRONOSOME-BASED FLATFORMS
TITLE OF INVENTION: CHRONOSOME-BASED PLATFORMS
FILE REFERENCE: 24601-420
CURRENT APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR PLILING DATE: 2002-05-30
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.0
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 56, Application US/10161403
Publication No. US20030119104A1
GENERAL INFORMATION: Edward
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Brasch, Michael A.
Temple, Gary F.
Hartley, James L.
Byrd, Devon R.N.
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ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative
                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) OTHER INFORMATION: attP2,P3 US-10-161-403-56
                                                                                                                                                                                                                                                 FEATURE:
CTHER INFORMATION: attR3
US-10-161-403-51
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US-09-732-914-10
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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LENGTH: 25
                                                                                                                                                                                                     TYPE: DNA
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  Publication No. US200300587222.
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                             NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.6%; Score 23.4; DB 14; Length 25; 96.0%; Pred. No. 1.1;
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                                                                                                                                                                                                                                                                               STATE: DC.
COUNTRY: USA
ZIP: 200334
ZIP: 200334
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC Compatible
COMPUTER: ISM PC Compatible
OPERATURG SYSTEM: PC-DOS/WS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Fleming, Elena
APPLICANT: Stewart, Sandra
APPLICANT: Stewart, Joan
TITLE OF INVENTION: CHROMSSOME-BASED PLATFORMS
FILE REFERENCE: 24601-420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/162,879
FILING DATE: 06-Unn-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
FILING DATE: «Unknown»
APPLICATION NUMBER: 09/05,476
FILING DATE: 10-UAN-1999
APPLICATION NUMBER: 09/05,476
FILING DATE: 12-UAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UN-1996
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UN-1996
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UN-1996
TELECOMMUNICATION INFORMATION:
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MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-162-879-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/161,403 CURRENT FILING DATE: 2002-05-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GTTCAGCTTTTTTGTACAAGTTGG 25
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; Sequence 51, Application US/10161403
; Publication No. US20030119104A1
; Publication No. Perkins,
; APPLICANT: Perkins, Edward
; APPLICANT: Perkins, Edward
; APPLICANT: Lindenbaum, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Greene, Amy
Leung, Josephine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.0°
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
APPLICANT:
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APPLICANT:
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Gaps

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                                                                             Gaps
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Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
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                                Length 25;
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                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/162,879
                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX,
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23.4; DB 14;
Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 06-Unn-2002
CLASSIFICATION: «Unknown»
PRIOR APPLICATION: «Unknown»
APPLICATION NUMBER: US/09/422,085
FILING DATE: «Unknown»
APPLICATION NUMBER: 09/033,493
FILING DATE: 20-UNN-1999
APPLICATION NUMBER: 09/05,476
FILING DATE: 12-UNN-1996
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UNN-1996
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UNN-1996
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UNN-1995
TELECOMMUNICATION: NUMBER: 08/486,139
FILING DATE: 07-UNN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches
                                                                               0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 11:
                                     Score 23.4;
Pred. No. 1.
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US-10-162-879-16
; Sequence 16, Application US/10162879
                                                                                                                                                                                                                                                                              Sequence 11, Application US/10162879; Publication No. US20030068799A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.6%;
                                     Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative
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Best Local Similarity 96.0
Matches 24; Conservative
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US-10-058-292-16
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Brasch, Michael A.
TITLE OF INVENTION: Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                          .
0
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CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                  Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,292
FILING DATE: 30-Jan-2002
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION: <UNKnown>
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 09/432,085
                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                              93.6%; Score 23.4; DB 14;
ilarity 96.0%; Pred. No. 1.1;
Conservative 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-2NN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 16:
       FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/406,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                              TOPOLOGY: both

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-10-058-292-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                         25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTICAGCTITTTTGTACAAAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: USA
ZIP: 20065-3934
COMPUTER READDBLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 16, Application US/10058292; Publication No. US20030054552A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 24; Conserv
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US-10-058-292-16
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RESULT 33
US-10-055-001A-11
US-10-055-01A-11
Sequence 11, Application US/10055001A
Publication No. US2030049835A1
GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Weterhouse, Peter
APPLICANT: Helliwell,Christopher A.
TITLE OF INVENTION: Nethod and means for producing efficient silencing constructs;
TITLE OF INVENTION: Number of Management of Policy Price Constructs;
FILE REFERENCE: HELLGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
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Gaps
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
   Indels
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ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX,
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 23.4; DB 14;
Pred. No. 1.1;
0; Mismatches 1;
      7;
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CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/432,085
FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
   0; Mismatches
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10-058-292-11

Sequence 11, Application US/10058292

Publication No. US20030054552A1

GENERAL INFORMATION:

APPLICANT: Hartley, James L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCUNTRY: USA
ZETP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                               1 GITCAGCITITITIGIACAAAGITGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.6%;
96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 96.09
Matches 24; Conservative
      Conservative
            24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 25
            Matches
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APPLICANT: Materhouse, Peter
APPLICANT: Materhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Nethod and means for producing efficient silencing constructs
TITLE OF INVENTION: Uning recombinational cloning
FILE REFERENCE: HELLGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 25
                                                                                                                                                                                                                                                                                            US-10-300-892-16

Sequence 16, Application US/10300892

Sequence 16, Application US/10300892

Sequence 16, Application No. US20030175970A1

Sequence 16, Application No. US20030175970A1

SERICANT: Hartley, James L.

APPLICANT: Hartley, James L.

APPLICANT: Temple, Gary F.

APPLICANT: Femple, Gary F.

APPLICANT: Femple, Gary F.

APPLICANT: Recombinational Cloning Using Nucleic Acids Having

TITLE OF INVENTION: Recombination Sites

TITLE OF INVENTION: 1201-07-19

PRIOR FILING DATE: 1998-10-23

NUMBER: OF SEQ ID NOS: 60

SEQ ID NO 16

LENGTHE DATE: 125

LENGTHE DATE: 20

LENGTHE DATE: 2
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                                                                                                         Gaps
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; OTHER INFORMATION: core sequence of recombination site attR3
US-10-055-001A-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 25;
                                                Score 23.4; DB 12; Length 25; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 23.4; DB 12;
Pred. No. 1.1;
0; Mismatches 1;
                                                                                                                0; Mismatches
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APPLICANT: Wesley, Susan V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            93.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 93.6%;
Best Local Similarity 96.0%;
Matches 24; Conservative (
                                                   ch 93.6%;
1 Similarity 96.0%;
24; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 32
US-10-055-001A-6
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Best Local
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Matches
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US-09-985-448-16;
Sequence 16, Application US/09985448
Sequence 16, Application US/09985448
Sequence 16, Application US/09985448
Sublication No. US20030157716A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REPERENCE: 0942.885004
CURRENT APPLICATION NUMBER: US/09/985,448
CURRENT APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 2001-11-02
PRIOR FILING DATE: 1998-10-23
PRIOR FILING DATE: 1998-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 16
LEAST SECTION OF SEQ ID NOS: 60
SEQ ID NO 16
LEAST SECTION OF SEQ ID NOS: 60
SEQ ID NO 16
LEAST SECTION OF SEQ ID NOS: 60
SEQ ID NO 16
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ORGANISM: Unknown
FEBATURE:
OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
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93.6%; Score 23.4; DB 11; Length 25;
Best Local Similarity 96.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 1; Indels (
MEDIUM TYPE: Floppy disk
COMPUTER: IBW PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
FILING DATE: (Herewith)
CLASSIFICATION: APPLICATION DATA:
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
CLASSIFICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
CLASSIFICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 20-311-2600
TELEPRANCE: 202-311-2600
TELEBRANCE: 202-311-2600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-985-448-16
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US-09-16
is Sequence 16, Application US/09432085
j Publication No. US2003010110A1
graphication No. US2003010110A1
j APPLICANT: Hartley, James L.
j APPLICANT: Brasch, Michael A.
j TITLE OF INVENTION: Recombinational Cloning Using Engineered
j TITLE OF INVENTION: Recombination Sites
j CORRESPONDENCE ADDRESS:
j CORRESPONDENCE ADDRESS:
j CORRESPONDENCE ADDRESS:
j STREET: 1100 New York Ave., N. W. Suite 600
j STATE: DC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  93.6%; Score 23.4; DB 11; Length 25; 96.0%; Pred. No. 1.1;
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                                                                                                                           ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
CIIY: Waghington
                                                                                                                                                                                                                              COUNTRY: WGA

ZITE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
FILING DATE: (Herewith)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: 09/663,002
FILING DATE: 12-UNN-1998
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UNN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UNN-1996
CLASSIFICATION:
PRIOR APPLICATION NUMBER: 08/663,002
FILING DATE: 07-UNN-1996
CLASSIFICATION NUMBER: 08/486,139
FILING DATE: 07-UNN-1995
CLASSIFICATION NUMBER: 07-UNN-1995
FILING DATE: 07-UNN-1995
CLASSIFICATION:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-UNN-1995
CLASSIFICATION: UNDER: 07-UNN-1995
FILING DATE: 07-UNN-1995
CLASSIFICATION: UNDER: 07-UNN-1995
FILING DATE: 07-UNN-1995
CLASSIFICATION: UNDER: 07-UNN-1995
CLASSIFICATION: UNDER: 07-UNN-1995
FILING DATE: 07-UNN-1995
CLASSIFICATION: UNDER: 07-UNN-1995
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                                         IIILE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CARRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GTTCAGCTTTTTGTACAAGTTGG 25
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TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFRX: 202-371-453-7
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
TRNGTH: 25 base pairs
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Best Local Similarity 96.0°
Matches 24; Conservative
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COMPUTER READABLE FORM:
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STRANDEDNESS: both
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1 GTTCAGCTTTTTGTACAAAGTTGG 25
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96.0%;
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96.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Unknown
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US-09-432-085-11
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APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having;
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850008
CURRENT APPLICATION NUMBER: 05/286,797A
CURRENT APPLICATION NUMBER: 09/286,281
PRIOR PILING DATE: 1999-04-22
PRIOR PLING DATE: 1999-04-22
PRIOR PLING DATE: 1997-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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FEATURE:
ORGENISM: CORGANISM: CORGANISM: recombination
OTHER INFORMATION: products
US-09-855-797A-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 93.6%; Score 23.4; DB 9; Length 25; Best Local Similarity 96.0%; Pred. No. 1.1; Matches 24; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          squence 8, Application US/09822634
patent No. US20201505561
GENERAL INFORMATION:
APPLICANT: Vile, Richard G.
APPLICANT: Bateman, Andrew
APPLICANT: WINSWITION: COMPOSITIONS AND METHODS FOR TISSUE
TITLE OF INTENTION: COMPOSITION SPECIFIC GENE REGULATION THERAPY
FILE REFERENCE: 07039-289001
CURRENT FILING DATE: 2001-03-30
PRIOR APPLICATION NUMBER: 60/193,977
PRIOR PILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FaetSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
; OTHER INFORMATION: Synthetically generated vector sequence
US-09-822-634-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTTCAGCTTTTTTGTACAAGTTGG 25
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APPLICANT: Hartley, James L. APPLICANT: Brasch, Michael A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Artificial Sequence
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Sequence 16, Application US/09907719

Sequence 16, Application US/09907719

Publication No. US20020192819A1

GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REPERENCE: 0942.2850004

CURRENT APPLICATION NUMBER: US/09/907,719

CURRENT FILING DATE: 2001-07-19

PRIOR FILING DATE: 1998-10-23

NUMBER OF SEQ ID NOS: 60

SOUTHYRRE: PATCHILL VET. 2.0
AFFLICANT: FOX, Donna K.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: 08/09/907,900
CURRENT FILING DATE: 2001-07-19
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 16
LENGTH: 25
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OTHER INFORMATION: Description of Unknown Organism: recombination
OTHER INFORMATION: products
                                                                                                                                                                                                                                                                                                                                                 FEATURE:
JOTHER INFORMATION: Description of Unknown Organism: recombination
JOTHER INFORMATION: products
US-09-907-900-16
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Publication No. US20030100110A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
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Pred. No. 1.1;
0; Mismatches 1;
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Pred. No. 1.1;
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TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850064
CURRENT APPLICATION NUMBER: US/09/985,448
FUNERNY FILING DATE: 102.
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
PRIOR PRILING DATE: 1998-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 43, Application US/10300892; Publication No. US20030175970A1; GENERAL INFORMATION:
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Best Local Similarity 88.0
Matches 22; Conservative
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Matches 22; Conservative
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ORGANISM: Unknown
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; Sequence 43, Application US/09907719
; Sequence 43, Application US/09907719
; Publication No. US20020192819A1
; Publication No. US20020192819A1
; Publication No. US20020192819A1
; APPLICANT: Braech, Michael A.
    APPLICANT: Temple, Gary F.
    APPLICANT: Temple, Gary F.
    APPLICANT: Pox, Donna K.
    TITLE OF INVENTION: Recombination Sites
    TITLE OF INVENTION: Recombination Sites
    TITLE OF INVENTION: Recombination Sites
    FILE REFERENCE: 0942.2850004
    CURRENT APPLICATION NUMBER: US/09/907,719
    CURRENT FILING DATE: 1998-10-23
    NUMBER OF SEQ ID NOS: 60
    SOFTWARE: PatentIn Ver. 2.0
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 43
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18-09
       TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites FILE REFERENCE: 0942.2850004 across CURRENT APPLICATION NUMBER: US/09/907,900 CURRENT FILING DATE: 2001-07-19 PRIOR APPLICATION NUMBER: 09/177,387 PRIOR FILING DATE: 1998-10-23 NUMBER OF SEQ ID NOS: 60 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 43 LENGTH: 25
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US-08-907-719-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; OTHER INFORMATION: Description of Unknown Organism: recombination: OTHER INFORMATION: products
US-09-907-900-43
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Best Local Similarity 88.0°
Matches 22; Conservative
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ORGANISM: Unknown
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APPLICANT: Hartley, James L.
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
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OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
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                                                                                                 95.2%; Score 23.8; DB 12; BB.0%; Pred. No. 0.73; cive 3; Mismatches 0;
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CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/907,719
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: 25
LENGTH: 25
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Sequence 43, Application US/09855797A

Patent No. US20020094574A1

GENERAL INFORMATION:
APPLICANT: Bratley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombination Sites
FILER REPERENCE: 0942.2850008

CURRENT APPLICATION NUMBER: US/09/855,797A

CURRENT APPLICATION NUMBER: US/09/855,797A

CURRENT FILING DATE: 1999-04-22

PRIOR PILING DATE: 1999-04-22

PRIOR FILING DATE: 1999-10-24

PRIOR FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 60

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 43

LENGTH: 25

TYPE: DNA

ORGANISM: UNKNOWN

PRANCE OF SEQ ID NOS: 60

SPANCE OF SEQ ID NOS: 60

SEQ ID NO 43

CENTRE OF SEQ ID NOS: 60

SEQ ID NO 43

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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COTHER INFORMATION: Description of Unknown Organism: recombination
COTHER INFORMATION: products
COL-09-855-797A-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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Best Local Similarity 100.0%; Score 25; DB 14; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
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95.2%; Score 23.8; DB 9; Length
Best Local Similarity 88.0%; Pred. No. 0.73;
Matches 22; Conservative 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                       FEATURE:
NAME/KRY: misc_feature
NAME/KRY: (1443)..(2148)
OTHER INFORMATION: nopaline synthase gene terminator
NAME/KEY: misc feature
LOCATION: (264)..(496)
OTHER INFORMATION: nopaline synthase gene promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc_feature

| LOCATION: (2149)..(2706)

| OTHER INFORMATION: a left T-DNA border region

US-10-055-001A-13
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                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (497)...(1442)
OTHER INFORMATION: nptII coding region
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) Sequence 43, Application US/09907900

) Patent No. US20020172997A1

) GENERAL INFORMATION:

APPLICANT: Hartley, James L.

; APPLICANT: Brasch, Michael A.

; APPLICANT: Temple, Gary F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 20
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                                                                                                                           US-10-055-01A-13/C
US-10-055-01A-13/C
Sequence 13, Application US/10055001A
Sequence 13, Application WS/10055001A
Publication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Wesley, Susan V.
APPLICANT: Wesley, Euch
APPLICANT: Wesley Pecr
APPLICANT: Wesley Pecr
APPLICANT: Wesley Wesley
APPLICANT: Wesley
APPLICANTON: Using recombinational cloning
FILE REFRENCE: HELAGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Version 3.1
SEQ ID NO 13
LENGTH 18691
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LOCATION: (17922)..(18687)
OTHER INFORMATION: octopine synthase gene terminator region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (16551)...(16319)
OTHER INFORMATION: attP2 recombination site (complement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: misc_feature
LOCATION: (17890)..(17659)
OTHER INFORMATION: attP1 recombination site (complement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (13675)..(13980)
OTHER INFORMATION: ccdB selection marker (complement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc feature
LOCATION: (17610)..(16855)
OTHER INFORMATION: ccdB selection marker (complement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (15002)..(15661)
OTHER INFORMATION: chloramphenicol resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc feature
LOCATION: (10706)..(11324)
OTHER INFORMATION: right T-DNA border fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: acceptor vector PHELLSGATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
NAME/KEY: (13048)..(13279)
OTHER INFORMATION: attPl recombination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (11674)..(13019)
OTHER INFORMATION: CAMV35S promoter fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (14387)..(14619)
OTHER INFORMATION: attP2 recombination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: misc feature
LOCATION: (7922)..(9985)
OTHER INFORMATION: spectinomycin resistance
               17792 GITCAGCITITITGIACAAAGIIGG 17816
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LOCATION: (14660)..(16258)
OTHER INFORMATION: pdk2 intron 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial sequence
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Best Local Similarity 100.0%; Score 25; DB 14; Length 18691;
Best Local Similarity 100.0%; Pred. No. 0.74;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (17922)..(18687)
OTHER INFORMATION: octopine synthase gene terminator region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc feature
LOCATION: (16551)..(16319)
OTHER INFORMATION: attP2 recombination site (complement)
                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (17890)..(17659)
OTHER INFORMATION: attP1 recombination site (complement)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
LOCATION: (13675)..(13980)
OTHER INFORMATION: ccdB selection marker (complement)
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LOCATION: (1443)..(2148)
OTHER INFORMATION: nopaline synthase gene terminator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: (17610)..(16855)
OTHER INFORMATION: ccdB selection marker (complement)
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LOCATION: (264)..(496)
OTHER INFORMATION: nopaline synthase gene promoter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (15002)..(15661)
OTHER INFORMATION: chloramphenicol resistance gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEATURE:
NAME/FEXT: misc_feature
NAME/FEXT: misc_feature
CATION: (2149)..(2706)
OTHER_INFORMATION: a left T-DNA border region
                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (10706)..(11324)
OTHER INFORMATION: right T-DNA border fragment
INFORMATION: acceptor vector phellsGale
                                                                                                                                                                                                                                                                   NAME/KEY: misc feature
LOCATION: (11674)..(13019)
OTHER INFORMATION: CANV35S promoter fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc feature
LOCATION: (13048)..(13279)
OTHER INFORMATION: attP1 recombination site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: (14387)..(14619)
OTHER INFORMATION: attP2 recombination site
                                                         NAME/KEY: misc_feature
LOCATION: (7922)..(9985)
OTHER INFORMATION: spectinomycin resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GTTCAGCTTTTTGTACAAAGTTGG 25
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NAME/KEX: misc feature
LOCATION: (497).. (1442)
OTHER INFORMATION: npt11 coding region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc feature
LOCATION: (14660)..(16258)
OTHER INFORMATION: pdk2 intron 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc feature
LOCATION: (17610)..(16
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US-10-055-001A-23/c

US-10-055-001A-23/c

SQUENCE 23, Application US/10055001A

Publication No. US20030049835A1

GENERAL INFORMATION:

APPLICANT: Wesley, Susan V.

APPLICANT: Wesley, Deter

APPLICANT: Wetchouse, Peter

APPLICANT: Helliwell, Christopher A.

APPLICANT: Helliwell, Christopher A.

TITLE OF INVENTION: Method and means for producing efficient silencing constructs

TITLE OF INVENTION: Using recombinational cloning

FILE REFERENCE: 1000 and MEDICALION UNMERS. US/10/055,001A

CURRENT PILLING DATE: 2002-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PatentIn version 3.1

SEQ ID NO 23

LENGTH: 17862
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APPLICANT: Wesley, Susan V.
APPLICANT: Wesley, Susan V.
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE OF INVENTION: Wind recombinational cloning
FILE REFERENCE: HELLGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
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100.0%; Score 25; DB 14; Length 17862;
Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
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0
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Best Local Similarity 100.0%; Pred. No. 0.73;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
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US-10-055-001A-23
                                                                                                                                                                     TYPE: DNA
CRGANISM: Artificial sequence
FRATURE:
FRATURE:
COMPACION: acceptor vector phelisGate4
US-10-055-001A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13146 GTTCAGCTTTTTGTACAAGTTGG 13122
             CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 23
LENGTH: 17862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16963 GTTCAGCTTTTTGTACAAGTTG 16987
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US-10-055-001A-13
Sequence 13, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial sequence
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LENGTH: 18691
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Gaps

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APPLICANT: CHEO, DAVID
APPLICANT: LI, XIAO
APPLICANT: LI, XIAO
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: ESPOSITO, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
FILE REPERENCE: 0942-512001
CURRENT FILING DATE: 2002-05-21
PRIOR PILING DATE: 2002-05-21
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ 1D NOS: 64
SEQ ID NOS: 64
SEQ ID NOS: 64
SEQ ID NO 61
LENGTH: 5584
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APPLICANT: Wesley, Susan V.
APPLICANT: Wesley, Deter
APPLICANT: Helliwell, Christopher A.
TITILE OF INVENTION: Method and means for producing efficient silencing constructs
TITILE OF INVENTION: using recombinational cloning
FILE REFERENCE: HELLGA
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Best Local Similarity 100.0%; Pred. No. 0.59;
Matches 25; Conservative 0; Mismatches 0; Indels 0
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100.0%; Pred. No. 0.57;
tive 0; Mismatches 0; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: plasmid pDONR207
US-10-151-690-61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 61, Application US/10151690
Publication No. US20030124555A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BRASCH, MICHAEL A. APPLICANT: CHEO, DAVID
                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 25; Conservative
                                                                        NAME/KEY: gene
LOCATION: (2210)..(2442)
OTHER INFORMATION: attP2
                                                                                                                              OTHER -
FEATURE:
NAME/KEY: gene
'.(3374)
                                                                                                                                                                                                                                                                             ..(4134)
LOCATION: (1303)..(1962)
OTHER INFORMATION: CMR
                                                                                                                                                                                                                                                       NAME/KEY: gene

LOCATION: (3495)..(413-

COTHER INFORMATION: ori

US-10-151-690-21
                                                                                                                                                                                           LOCATION: (2565)..(337.OTHER INFORMATION: Kmr
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                                                       FEATURE:
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                                                                                         GENERAL INCOMPATION:
APPLICANT: DRAWLICH.
APPLICANT: CHEO. DAVID
APPLICANT: CHEO. DAVID
APPLICANT: CHEO. DAVID
APPLICANT: ESPOSITO.
APPLICANT: ESPOSITO.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOLY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOLY
TITLE OF ILING DATE: 2002-05-21
CURRENT FILING DATE: 2002-05-21
PRIOR FILING DATE: 2002-05-21
PRIOR PLILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOCTHARE: PALENTEN WEBSE: 301-05-21
NUMBER OF SEQ ID NOS: 64
SEQ ID NO 30
LENGTH: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: LI, XIAO
APPLICANT: LI, XIAO
APPLICANT: ESPOSITO, DOWINIC
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOL
FILE REFERENCE: 0942.5120001
CURRENT APPLICATION NUMBER: US 10/151,690
PRIOR FILING DATE: 2002-05-21
PRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARR: PARENTING PARE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SOFTWARR: PARENTIN VERSION 3.1
SEQ ID NO 21
LENGTH: 4470
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 21, Application US/10151690
Publication No. US20030124555A1
GENERAL INFORMATION:
APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
                        Application US/10151690 No. US20030124555A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: gene
LOCATION: (29)..(260)
OTHER INFORMATION: attPl
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LOCATION: (1099)...(1184)
OTHER INFORMATION: ccdA
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LOCATION: (656)..(961)
OTHER INFORMATION: ccdB
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Best Local Similarity
Matches 25; Conserv
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NAME/KEY: gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: attPl
US-10-151-690-30
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APPLICANT: Leung, Josephine
APPLICANT: Eleming, Josephine
APPLICANT: Slewart, Sandra
APPLICANT: Shewlart, Sandra
APPLICANT: Shewlart, Sandra
APPLICANT: Shellard, Joan
TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILE REFERENCE: 24601-420
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT FILING DATE: 2002-05-30
PRIOR APPLICATION NUMBER: 60/294,758
PRIOR APPLICATION NUMBER: 60/366,891
PRIOR FILING DATE: 2002-03-21
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FastSEQ for Windows Version 4.C
SEQ ID NO 55
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GITCAGCTITITIGIACAAAGIIGG
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: Perkins, Eawa...

: Perez, Carl

T: Lindenbaum, Michael

VT: Greene, Amy

VT: Greephine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25; Conservative
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Best Local Similarity 100.0
Matches 25; Conservative
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Best Local Similarity
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US-09-732-914-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
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                                                                            Gaps
                                                                                                                                                                                                                                                                                                          ublication No. working the CENERAL INFORMATION:
APPLICANT: Hartley, James L.
Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered Recombination Sites
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0
                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSER: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 25; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTER TEACHER TO COUNTER TEACHER TO COUNTER TEACHER FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTER: PC-DOS/MS-DOS
SOFTWARE: PATENTER: PATENTER: PATENTER: PATENTER: PATENTER: PATENTER: OS-Jun-2002
CLASSIFICATION NUMBER: US/10/162,879
FILING DATE: OS-Jun-2002
CLASSIFICATION NUMBER: US/09/432,085
FILING DATE: CURKNOWN>
APPLICATION NUMBER: 09/05,476
FILING DATE: 12-JAN-1999
APPLICATION NUMBER: 09/05,476
FILING DATE: 12-JAN-1999
APPLICATION NUMBER: 08/663,002
FILING DATE: 12-JAN-1999
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELECOMMUNICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
                               DB 14; Length 25;
                                                                            0; Indels
                                                  0.22;
                            Query Match
100.0%; Score 25; DB
Best Local Similarity 100.0%; Pred. No. 0.2
Matches 25; Conservative 0; Mismatches
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SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-162-879-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GTTCAGCTTTTTGTACAAGTTGG 25
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                                                                                                                                                 1 GTTCAGCTTTTTGTACAAAGTTGG 25
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US-10-162-879-15
Sequence 15, Application US/10162879
; Publication No. US20030068799A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δ
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APPLICANT: Chee, David
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, Michael A.
APPLICANT: Brasch, James L.
APPLICANT: Hartley, James L.
APPLICANT: Byrd, Devon R.N.
TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity ir
TITLE OF INVENTION: Recombinational Cloning
FILE REFERENCE: 0942.501002
CURRENT APPLICATION NUMBER: US/09/732,914
CURRENT FILING DATE: 2000-12-11
PRIOR APPLICATION NUMBER: US 60/169,983
PRIOR FILING DATE: 1999-12-10
PRIOR APPLICATION NUMBER: US 60/169,083
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 140
SEQ ID NOS: 140
SEQ ID NO 6
IENGTH: 27
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100.0%; Score 25; DB 14; Length 25; 100.0%; Pred. No. 0.22; tive 0; Mismatches 0; Indels
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RESULT 12 US-10-151-690-30

Sequence 55, Application US/10161403 Publication No. US20030119104A1 GENERAL INFORMATION:

US-10-161-403-55

RESULT 10

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using recombinational cloning
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; MOLECULE TYPE: CDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-058-292-15
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                                                                                                                                                                                                              ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
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                                                                                                                                                                                         TYPE: DNA
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APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.

IIILE OF INVENTION: Method and means for producing efficient silencing constructs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·
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; Sequence 15. Application US/20030175970A1
; Publication No. US20030175970A1
; GENERAL INFORMATION:
; APPLICANT: Brasch, Michael A.
; APPLICANT: Temple, Gary F.
; APPLICANT: Temple, Gary F.
; APPLICANT: Temple, Gary F.
; TITLE OF INVENTION: Recombination Sites
; TITLE OF INVENTION NUMBER: US/09/907,719
; PRIOR FILING DATE: 1098-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
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                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 12; Length 25; 100.0%; Pred. No. 0.22; cive 0; Mismatches 0; Indels
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100.0%; Pred. No. 0.22;
ative 0; Mismatches 0;
  CURRENT APPLICATION NUMBER: US/09/985,448

CURRENT FILING DATE: 2001-11-02

PRIOR APPLICATION NUMBER: US/09/177,387

PRIOR FILING DATE: 1998-10-23

PRIOR APPLICATION NUMBER: US 60/065,930

PRIOR PILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 60

SOFTWARE: PALENTIN Ver. 2.0

SEQ ID NO 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTCAGCTTTTTTGTACAAGTTGG 25
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Sequence 10, Application US/10055001A
; Publication No. US20030049835A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Descript.; OTHER INFORMATION: products US-10-300-892-15
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 25; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Unknown
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Unknown
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Gaps
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Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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; OTHER INFORMATION: core sequence of recombination site attP1
US-10-055-001A-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION MARBRE: US/10/058,292
FILING DATE: 30-Jan-2002
CLASSIFICATION: <Unknown>
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CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX,
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
100.0%; Score 25; DB 14;
Best Local Similarity 100.0%; Pred. No. 0.22;
Matches 25; Conservative 0; Mismatches 0;
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APPLICATION NUMBER: 09/432,085
FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1999
APPLICATION NUMBER: 09/63,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1995
TELECATION NUMBER: 08/486,139
TELECATION NUMBER: 08/486,139
TELECATION NUMBER: 208-371-2600
TITLE OF INVENTION: using recombinational FILB REFRENCE; HELLGA CURRENT APPLICATION NUMBER: US/10/055,001A CURRENT FILING DATE: 2002-06-11 NUMBER OF SEQ ID NOS: 26 SOFFWARE: Patentin version 3.1 SEQ ID NO 10 DO                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTTCAGCTTTTTTGTACAAAGTTGG 25
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Publication No. US20030054552A1
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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US-09-985-448-15
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Publication No. US20020192819A1
GENERAL INFORMATION;
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/09/907,719
CURRENT FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PALENTIN OF: 2.0
SOFTWARE: PALENTIN Ver. 2.0
SEQ ID NO 15
INDIGHT: 25
                                                                             GENERAL INFORMATION:
APPLICANT: Hartley, James I.
APPLICANT: Hartley, James I.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION Recombination Sites
FILE REFERENCE: 0942.255.0004
CURRENT FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: 09/177,387
PRIOR APPLICATION NUMBER: 09/177,387
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
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CTHER INFORMATION: Description of Unknown Organism: recombination
CHER INFORMATION: products
CHER 19-19-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Description of Unknown Organism: recombination; OTHER INFORMATION: products
US-09-907-900-15
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100.0%; Pred. No. 0.22;
iive 0; Mismatches 0;
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                Sequence 15, Application US/09907900 Patent No. US20020172997A1 GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 25; Conservative
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Best Local Similarity 100.
Matches 25; Conservative
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Unknown
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US-09-907-719-15
US-09-907-900-15
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Sequence 15, APPLication US/0942085

DEREAL INFERDATION: 10.10.04

PREJIGNT: Brasch, Michael A.

TITLE OF INVENTION: Recombination Sites

NUMBER OF SEQUENCES: 35

CORRESPONDED AND RECOMBINATION SITES

NUMBER OF SEQUENCES: 35

CORRESPONDED AND RECOMBINATION SITES

CONDITY: Washington With States and States a
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RESULT 4 US-09-432-085-15 н

Sequence 16, Appl.
Sequence 16, Appl.
Sequence 16, Appl.
Sequence 11, Appl.
Sequence 11, Appl.
Sequence 16, Appl.
Sequence 16, Appl.
Sequence 16, Appl.
Sequence 16, Appl. Sequence 56, App Sequence 10, Appl Sequence 43, Ap. Sequence 43, P. Sequence 43, P. Sequence 43, P. Sequence 43, Sequence 16, Sequence 8, Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence 4 US-10-055-001A-13 4 US-10-055-001A-13 US-09-957-97A-43 US-09-957-970-43 US-09-985-448-43 2 US-10-300-985-448-43 2 US-10-985-448-48 US-09-852-634-8 US-09-852-634-8 US-09-852-634-8 US-09-852-634-8 US-09-907-719-16 US-09-907-719-16 US-09-985-488-16 2 US-09-907-901-16 US-09-985-48-16 2 US-09-985-48-16 4 US-10-055-001A-11 4 US-10-058-292-16 4 US-10-058-292-16 4 US-10-162-879-16 4 US-10-161-403-56 US-09-732-914-10 US-09-732-914-10 US-09-732-914-10 US-09-732-914-10 US-10-161-403-56 US-10-161-403-56 US-10-151-690-62 4 US-10-151-690-63 4 US-10-151-690-63 

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RESULT 1
US-09-855-797A-15
Sequence 15, Application US/09855797A
Sequence 15, Application US/09855797A
Setent No. US20020094574A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary E.
TILLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
TILLE OF INVENTION: Recombination Sites
TILLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850008
CURRENT FILING DATE: 2001-05-16
PRIOR PLILING DATE: 1999-04-22
PRIOR PLILING DATE: 1999-04-22
PRIOR PLILING DATE: 1999-04-22
PRIOR FILING DATE: 1999-10-65, 330
PRIOR FILING DATE: 1999-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 15
LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: Description of Unknown Organism: recombination ; OTHER INFORMATION: products
US-09-855-797A-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
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Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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RESULT

Sequence 61, 8 Sequence 23, 8 Sequence 23, 8 Sequence 30, Sequence 21,

4470 5584 17862 17862

100.0

100.0 100.0

100.0

XX SQ Sequence 27 BP; 6 A; 5 C; 6 G; 10 T; 0 other;

Query Match 93.6%; Score 23.4; DB 25; Length 27; Best Local Similarity 96.0%; Pred. No. 1.2; Matches 24; Conservative 0; Mismatches 1; Indels 0; Gaps

0;

g ð

Search completed: November 6, 2003, 22:26:29 Job time : 111.5 secs

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The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, ENNA, structural prodeins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and proteins, vaccines, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistance to diseases insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that provides an agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The cherencologous nucleic acid optionally encodes a product that alters nutrient use and/or improves the nutrient quality of the plant. The cherencologous nucleic acid optionally encodes (YAC). This cherencosome (BAC) or a yeast artificial chromosome (YAC). This producing plant artificial chromosomes of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
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93.6%; Score 23.4; DB 25; 96.0%; Pred. No. 1.2; 0; Mismatches GTTCAGCTTTCTTGTACAAAGTTGG 25 1 GTTCAGCTTTTTTGTACAAAGTTGG 25 Local Similarity 96.0 nes 24; Conservative Query Match à

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Gaps

. 0

1;

Length 25; Indels

> AAS06183 standard; DNA; 27 BP RESULT 39

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12-SEP-2001 (first entry) AAS06183; 

Phage-lambda recombination site attP2

Bacteriophage lambda; recombination; att site; PCR primer; lambda Int; lambda integrase; therapeutic; ss.

Sacteriophage lambda

WO200142509-A1.

14-JUN-2001

11-DEC-2000; 2000WO-US33546

10-DEC-1999; 99US-0169983. 09-MAR-2000; 2000US-0188020.

CHEO D. CHEO/) BRAS/)

BRASCH M A. TEMPLE G F. (TEMP/) (HART/)

HARTLEY J L. BYRD D R N. (BYRD/)

Byrd DRN; Hartley JL, Temple GF, Brasch MA, 'n Cheo

WPI; 2001-356174/37

Producing hybrid nucleic acids, useful for expressing novel therapeutic polypeptides, by mixing the same or different nucleic acids having one or more recombination sites in the presence of recombination proteins,

Disclosure; Fig 24A; 357pp; English.

AAS06174-AAS06322 represent Bacteriophage lambda att recombination

ö att sequences are recognised by the recombination protein lambda integrates (Int). The invention is a new method of producing a population of hybrid nucleic acids comprising mixing at least a first population of nucleic acids comprising mixing at least a first population of nucleic acids comprising one or more recombination sites with at least one target nucleic acid comprising one or more recombination sites and causing some or all of the nucleic acids to recombination sites and the target nucleic acids. The method is useful for producing a population of hybrid nucleic acids which may be the same or different. The nucleic acids which may be the same or different. The nucleic may also be used to express therapeutic proteins or peptides and they may also be used to create novel fusion proteins by expressing different sequences linked to each other. The method allows simultaneous cloning of Gaps and PCR primers of the invention. The 0: Length 27; Indels Score 23.4; DB 22; Pred. No. 1.2; 0; Mismatches 1; Sequence 27 BP; 6 A; 5 C; 6 G; 10 T; 0 other; 1 GIICAGCITITIGIACAAGIIGG 25 Gricagciricirchicaaagrigg 25 two or more different nucleic acids. site nucleic acid sequences, th 93.6%; l Similarity 96.0%; 24; Conservative Local Similarity Query Match Matches RESULT 40 ABZ58736 à 원

ABZ58736 standard; DNA; 27 BP

(first entry) 01-MAY-2003

Att site nucleotide sequence attP2.

Nucleic acid insertion; recombination; nucleic acid selection; nucleic acid isolation; att; ds.

Synthetic.

WO200295055-A2

28-NOV-2002

21-MAY-2002; 2002WO-US15947. 

21-MAY-2001; 2001US-291973P.

(INVI-) INVITROGEN CORP

Byrd DRN; Esposito D, Li X, Cheo D, Brasch MA,

WPI; 2003-129436/12

Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid -

Disclosure, Fig 13A; 273pp; English.

The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid with a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. Sequences ABZSB727-762

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The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (I) a platform artificial chromosome expression system (ACes) (II) comprising several sites that participate in recombinated and several sites that participate in recombinated and allowed the participate introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for introducing a heterologous nucleic acid molecule into a platform a artificial chromosome, preferably an ACes. (II) is useful for producing a transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or mammal) by introducing (II) by cell fusion, lipid-mediated transfection by a carrier system, microinjection, microcall fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612 to ACC44712 and ABP96650 to ABP96657 represent sequences used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant artificial chromosome; PAC; transgenic plant; vaccine; blood factor; herbicide; stress; agronomical; nutrient quality; bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Artificial plant chromosome related oligo SEQ ID No 42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                          exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GTTCAGCTTTCTTGTACAAAGTTGG 25
                                     Claim 43; Page 143; 272pp; English.
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Best Local Similarity
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BP

Perkins E;

Gaps

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1; Indels

Length 25;

DB 25;

Score 23.4; D' Pred. No. 1.2; 0; Mismatches

93.6%; 96.0%;

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The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting insertion of heterologous DNA into plant artificial chromosomes, methods for delivery of plant chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transpenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, transpentic proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and proteins, receptors, antibodies, blood factors, antigens, hormones, cytokines, growth factors, antibodies, or a product that provides for resistance to diseases, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that alters nutrient use and/or improves the nutrient quality of the plant. The cheterologous nucleic acid proteins and within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (CAC). This producing plant artificial chromosomes of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plant artificial chromosome; PAC; transgenic plant; vaccine;
blood factor; herbicide; stress; agronomical; nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
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The present introduction describes a vector, (i) compliably operatory introduction on a recipient cell, preferably in bacteria such as Escherichia coli; (i) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a promoter region capable of being recognized by RNA polymerases of a chimeric DNA construct comprising: (i) promoter or region capable of being recognized by RNA polymerases of a chird and fourth recombination sites; (iii) 3' transcription terminating and polyademylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites, or sites are capable of reacting with a same recombination site, and corber or with a same recombination sites, or the third and fourth recombination sites, do not recombination sites, or the third and fourth recombination sites, do not recombination sites, or the third and fourth recombination sites. The vectors can also be used to producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to convent a DNA fragment into an invested repeat structure. Plants conventional breeding scheme to produce more plants with the same combination site attall which is given in the core sequence of recombination site attall which is given in the core exemplification of the present invention.
                                                                                                                                                                                        comprising operably linked
useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
                                                                                                                                                                                        present invention describes a vector (I) fragments having: (a) origin of replicati
                                                                                                                                     Page 15; 104pp; English.
                                                                                                                                        Claim 12;
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Score 23.4; DB 24; Length 25; Pred. No. 1.2; 0; Mismatches 1; Indels 25 25 1 GTTCAGCTTTTTTGTACAAAGTTGG 1 Gricagcrircrigiacaaagrigg ch 93.6%; l Similarity 96.0%; 24; Conservative ( Query Match Best Local Similarity Best Loca Matches Пр ð

ACC44660 standard; DNA; 25 29-MAY-2003 ACC44660; RESULT 35 ACC44660 

BP.

(first entry)

Recombination site related oligonucleotide SEQ ID NO:51.

att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; PCR primer; ss. Chromosome-based platform; artificial chromosome; eukaryotic chromosome;

Synthetic

WO200297059-A2.

05-DEC-2002

10-MAY-2002; 2002WO-US17452.

30-MAY-2001; 2001US-294758P. 21-MAR-2002; 2002US-366891P.

(CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

Fleming E; Leung J, Greene A, Lindenbaum M, Perez C, L Perkins E, Stewart S,

WPI; 2003-140461/13.

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The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (I) a platform artificial chromosome expression system (ACes) (II) comprising several sites that participate in recombination; and (2) a method (MI) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for chromosome. (I) can be used in gene therapy. (MI) is useful for chromosome, preferably an ACes. (II) is useful for producing a ratificial chromosome, preferably an ACes. (II) is useful for producing chromosome, microileic acid molecule into a platform of artificial chromosome, microileic acid molecule into an embryonic by a carrier system, microilection, microcell fusion, electroporation, microprojectile bombardment or direct DNA transfer into an embryonic microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for the codes at herapeutic product which is useful for the codes at the appeared product which is useful for the codes and AEPS of the AEPS of th
Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     exemplification of the present invention.
                                                                                                                                                                                                                                       Claim 43; Page 143; 272pp; English
                                                                                                                                                  interest
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Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;

Gaps . 0 Length 25; Indels Score 23.4; DB 25; Pred. No. 1.2; 1; 0; Mismatches 93.6%; 24; Conservative Query Match Best Local Similarity Matches

6

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Gaps

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RESULT 36 ACC44665

29-MAY-2003 (first entry) ACC44665;

ACC44665 standard; DNA; 25 BP

Recombination site related oligonucleotide SEQ ID NO:56.

Chromosome-based platform; artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; PCR primer; ss.

Synthetic.

WO200297059-A2. 

35-DEC-2002.

30-MAY-2002; 2002WO-US17452.

30-MAY-2001; 2001US-294758P. 21-MAR-2002; 2002US-366891P.

(CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

Leung J, Lindenbaum M, Greene A, Perez C, Li Shellard J; Perkins E, Stewart S, Stewart

Ξ,

WPI; 2003-140461/13.

Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of

Murphy S, Bateman A;

Harrington K,

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Core sequence of recombination site attR3 SEQ ID NO:6.
                                                                                                                                                                                         Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
(MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
                                                                                                                                                                                                                                                                                                                                                                                                    (CSIR ) COMMONWEALTH SCI & IND RES ORG.
                                                               Disclosure; Page 42; 84pp; English.
                                                                                                                                                                                                                                                                                                                                                                       24-JAN-2002; 2002WO-AU00073.
                                                                                                                                                                                                                                                                                                                                                                                  26-JAN-2001; 2001US-264067P.
29-NOV-2001; 2001US-333743P.
                                                                                                                                                                                                                                                                     ABQ82123 standard; DNA; 25
                                                                            invention relates to a
                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-682669/73.
                       WPI; 2001-656985/75
                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                               WO200259294-A1.
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                                                                                                                                                                                                                                                                                                                                                           01-AUG-2002
                                                    recombinase
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                                                                                                                                                                                                                                                                                ABQ82123;
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            Vile RG,
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24; Conservative

DB 23; Length 25; Indels

Ξ,

93.6%; Score 23.4; Di 96.0%; Pred. No. 1.2; :ive 0; Mismatches

1 GITCAGCTTTTTGTACAAGTTGG 25 Gricagcrircrigiacaaagrieg 25

(first entry)

Helliwell C;

Ω,

Waterhouse

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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coll; (b) selectable marker region capable of being expressed in the recipient cell, and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a cukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and polyadenylation region functional in the eukaryotic cell. The first correspond or recombination sites, or the second and third recombination site, and preferably are identical. The first and second recombination site, and the third and fourth recombination site, and second recombination site, or the third and fourth recombination site, and second recombination site, or the third and fourth recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for silencing target nucleic acid sequences. The vectors can also be used to silencing target nucleic acid sequences. The vectors can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence represents is given in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New vectors comprising operably linked DNA fragments having an origin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimaric gene for reduction of the phenotypic expression of mucleic acids. The present sequence of recombination site attBl which is given in the
New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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96.0%; Pred. No. 1.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exemplification of the present invention.
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                                                                                                                                              Disclosure; Page 15; 104pp; English
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29-NOV-2001; 2001US-333743P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 96.0%;
hes 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABQ82128 standard; DNA; 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-682669/73
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                              first expression cassette, comprising a first promoter operably linked to a nucleic acid sequence encoding a syncytium-inducing polypeptide (such as a fusogenic membrane glycoprotein) and flanked on either side by a comprising a tumour-specific promoter operably linked to a nucleic acid sequence encoding a recombinase, and/or a second expression cassette may be linked to a hypoxic response element (HRB), the second expression cassette may contain a promoter linked to a nucleic acid encoding a cytokine, and a third cassette may contain a tumour specific promoter linked to the nucleic acid encoding a cytokine, and a third cassette may contain a tumour specific promoter is, for example, a carcinoembryonic antigen (CEA) promoter or a tyrosinase promoter and the recombinase is, for example, cre recombinase or FLP recombinase. The invention is useful for reducing tumour size by administering the compositions as retroviral vectors, or in a cell containing the vector, to an individual in need of treatment for a disease caused by malignant cells. This sequence represents an Int
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                            Recombinant nucleic acid vector for reducing tumour size, has expression cassette comprises a promoter linked to nucleic acid sequence encoding a syncytium-inducing polypeptide and flanked on either side by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               for a disease caused by malignant cells. This sequence represents an Int
recombinase site core region attR3, required for excisive recombination
                                                                                                                                                                                                                                                                                                                                                                            recombinant nucleic acid vector comprising a
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The present invention describes an isolated nucleic acid molecule (I) comprising a first nucleic acid sequence having a defined sequence (AACSTS66 to AACSTS81, sequences complementary to AACSTS81, or an RNA sequence corresponding to AACSTS66 to AACSTS81, an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site or avoids hairpin formation, the recombination site obeing an att or lox site; (2) an isolated nucleic acid molecule (III) comprising a first att recombination site comprising a mutation site of the comprising a mutation that above mentioned nucleic acids; (3) vectors (IV) comprising the above mentioned nucleic acids or (IV). The nucleic acids are used in conjuncating a core region of a given recombination site to provide mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining engineered recombination in vitro or in vivo makes the methods for NNA or RNA subcloning, highly specific, rapid, and
                                                                                                                                                                                                                                                             Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank a selectable marker and comprise a core region having an engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli core region recombinant site attP2,P3 SEQ ID NO:16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Core region; recombination site; cloning; chimeric DNA; characteristic; mutation; att site; lox site; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                   Claim 1; Column 18; 73pp; English
                                                                                                                                                                (LIFE-) LIFE TECHNOLOGIES INC
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                                                                                                96US-0663002.
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Best Local Similarity 96.0
Matches 24; Conservative
                                                                                                                                                                                                   Brasch MA, Hartley JL;
                                                                                                                                                                                                                                 WPI; 2001-049004/06
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                                                                  20-JAN-1999;
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US6143557-A
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                                                                                                                                                                                                                                                                                                                       mutation
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Gaps

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The present invention describes an isolated nucleic acid molecule [1] comprising a first nucleic acid sequence having a defined sequence (AAC8786 to AAC87881, sequences complementary to AAC8786 to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87881. Also described are: (1) an isolated nucleic acid molecule [II] comprising a first mutated recombination site that removes one or more stop codons from the recombination site that removes one or more stop codons from the being an act or lox site; (2) an isolated nucleic acid molecule [II] comprising a first act recombination site comprising a mutation that comprising a first act recombination site comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids or [IV]. The nucleic acids are used in considering a core region of a given recombination site to provide mutative sites suitable for subcloning reactions. The use of nucleic acids for obtaining engineered recombination in vitro or in vivo makes the above methods for DNA or RNA subcloning, highly specific, rapid, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        syncytium-inducing polypetide; fusogenic membrane glycoprotein; tumour; tecombinase; tumour-specific promoter; hypoxic response element; HRB; ss; tyrosinase promoter; FLP; retroviral vector; malignant cell; cancer; excisive recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant nucleic acid vector; carcinoembryonic antigen; CEA; cytokine;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                   Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank selectable marker and comprise a core region having an engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lambda phage Int recombinase site core region DNA sequence attR3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93.6%; Score 23.4; DB 22; Length 25; 96.0%; Pred. No. 1.2; tive 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GITCAGCITITITGIACAAGTIGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GTTCAGCTTTCTTGTACAAAGTTGG
                                                                                                                                                                                                                                                                               Claim 1; Column 18; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                            (LIFE-) LIFE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAR-2001; 2001WO-US10250.
96US-0663002.
98US-0005476.
95US-0486139.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity 96.0
24; Conservative
                                                                                                               Brasch MA, Hartley JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         less labour intensive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriophage lambda.
                                                                                                                                                      WPI; 2001-049004/06
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   07-JUN-1996;
12-JAN-1998;
07-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                mutation
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ID AAS1
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31-MAR-2000; 2000US-193977P.

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Query Match

2 × 3

Matches

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The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors acch comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture; and selecting for a host comprising the chimeric nucleic acid molecule, and selecting gainst a host comprising the vectors conprising the second vector; to clone the nucleic acid. The present sequence is a recombinantion site, which may be used in the method of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli core region recombinant site attR3 SEQ ID NO:11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Core region, recombination site, cloning, chimeric DNA, characteristic, mutation, att site, lox site, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23.4; DB 22;
Pred. No. 1.2;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GITCAGCITITIGIACAAGIIGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gricagerirericiacia de 25
                                                                                                                                                                               Recombination site; cloning; att; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 25; Column 46; 73pp; English
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                  AAF55750 standard; DNA; 25 BP.
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Best Local Similarity 96.0%;
Matches 24; Conservative
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                                                                                                                                        Recombination site attP2,P3.
                                                                                                                                                                                                                                                                                                                                        98US-0005476.
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                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brasch MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-136877/14.
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                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                            US6171861-B1
                                                                                                                                                                                                                                                                                                                                        L2-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                07-JUN-1995;
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                                                                                                   12-APR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .nvention
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                                                           AAF55750;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host
                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          recombinantion site, which may be used in the method of the present
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                                                                                  Length 25;
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                                                                          Score 23.4; DB 22;
Pred. No. 1.2;
0; Mismatches 1;
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                                         Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GITCAGCITITITIGIACAAGTIGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTTCAGCTTTCTTGTACAAGTTGG 25
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                                                                                                                                                                                        GTTCAGCTTTCTTGTACAAAGTTGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombination site; cloning; att; ss.
                                                                                                                                                               1 GITCAGCITITITIGIACAAGTIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 25; Column 46; 73pp; English.
      useful for recombination cloning
                                                                                                                                                                                                                                                                                                       BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LIFE-) LIFE TECHNOLOGIES INC.
                                                                              Match 93.6%;
Local Similarity 96.0%;
les 24; Conservative
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95US-0486139.
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Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Recombination site attR3
                                                                                                                                                                                                                                                                                                       AAF55745 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hartley JL, Brasch MA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-136877/14.
                                                                                                                                                                                                                                                                                                                                                                                  12-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US6171861-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-JAN-1998;
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                                                                                                                                                                                                                                                                                                                                              AAF55745;
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RESULT 29

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Gaps

0;

Length 25; Indels

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The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NAMs) comprising: (a) combining in vitro or in vivo: (1) at least one insert donor molecules (IDMs) comprising one or more desired nucleic acid segments flanked by at least 2 comprising one recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMs) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or sites which do not recombine with each other; and (3) one or more of the site specific recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the composition of the desired product molecules (PMs). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides that methods can also be used for changing vectors. The oligonucleotides that methods can also be used for the method of the invention.
                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                              93.6%; Score 23.4; DI 96.0%; Pred. No. 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gricagcrircrigiacaaagrigg 25
                                                             Disclosure; Page 163; 185pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GTTCAGCTTTTTGTACAAGTTGG
                             nucleic acid cloning methods
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 96.0
WPI; 1999-303011/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US6270969-B1
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Matches
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Recombination site; copy number; replicon; recombinatorial cloning; Recombination site attR3 DNA 95US-0486139. 99US-0233492. 96US-0663002. AAD14439 standard; DNA; 25 (first entry)

(INVI-) INVITROGEN CORP.

Hartley JL, Brasch MA;

WPI; 2001-488248/53.

Methods for apposing nucleic acids comprising an expression signal ar a gene/partial gene, using recombinatorial cloning by incubating the nucleic acids in the presence of a recombination protein under conditions for recombination

The invention relates to a method for apposing an expression signal and a gene or partial gene, using recombinatorial cloning. The method incubates nucleic acids comprising the expression signal and the gene/partial gene in the presence of a recombination protein under conditions sufficient to cause recombination and therefore appose the expression signal and the gene or partial gene. The methods are useful for apposing an expression spinal and a gene or partial gene using recombinatorial cloning. The methods are also useful for changing vectors, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages, and cloning e.g., PCR products (with an attB site at one end and a loxP site at the other end), genomic DNAs, and cDNAs. The methods are highly specific, rapid, and less labour intensive than prior art methods. The present sequence is a recombination site

Claim 14; Column 18; 76pp; English

The invention relates to a method for apposing an expression signal and a gene or partial gene, using recombinatorial cloning. The method incubates nucleic acids comprising the expression signal and the gene/

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partial gene in the presence of a recombination protein under conditions signal and the gene recombination and therefore appose the expression signal and the gene or partial gene. The methods are useful for apposing an expression signal and a gene or partial gene using recombinatorial cloning. The methods are also useful for changing rectors, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages, and cloning e.g., PCR products (with an attB site at one end and a loxP site at the other end), genomic DNAs, and cDNAs. The methods are highly specific, rapid, and less labour intensive than brior att methods. The present sequence is a recombination site useful for recombination cloning.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Methods for apposing nucleic acids comprising an expression signal ar
a gene/partial gene, using recombinatorial cloning by incubating the
nucleic acids in the presence of a recombination protein under
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0
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                                                                                                                                                                                               Score 23.4; Di
Pred. No. 1.2;
                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                           1 GIICAGCIIICIIGIACAAGIIGG 25
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                                                                                                                                                                                                                                                      GTTCAGCTTTTTTGTACAAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombination site attP2, P3 DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conditions for recombination
                                                                                                                                                                                               93.6%;
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95US-0486139.
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                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                         24; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unidentified
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Gaps

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0; Mismatches 25

Length 25; Indels

DB 20;

WO9640724-A1

Synthetic.

19-DEC-1996

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         more nucleic acid molecules (MMEs) comparising: (a) combining in vitro or in vivo. (1) at least one insert donor molecules (IDMS) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMS) comprising at least 2 recombination sites which do not recombine with each other; add (3) one or more sites which control recombine with each other; and (3) one or more of transfer one or more of the desired segments into one or more of the VDMS, thereby producing no remore desired product molecules (PMS). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that have the desired characteristics and/or nucleic acid segments. The have the desired for charging vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to novel methods for cloning or subcloning one or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  att recombination site; core region; mutation; enhance; recombination; vector; subcloning; regulation; exchange; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                  Oligonucleotide #43 for recombination and cloning method.
                                                                                                                                                Cloning; donor; recombination site; vector; chimeric; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seguence 25 BP; 4 A; 3 C; 5 G; 10 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                               Temple GF;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTICAGCITITIGIACAAAGTIGG 25
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                                                                                                                                                                                                                                                                                                                                                                               Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                      New nucleic acid cloning methods
                            AAX78977 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                               (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 95.2%;
Local Similarity 88.0%;
les 22; Conservative
                                                                                                                                                                                                                                                                                                    98US-0177387.
97US-0065930.
                                                                                                                                                                                                                                                                       98WO-US22589
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                                                                                         17-AUG-1999 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                Fox DK,
                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-303011/25
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                                                                                                                                                                                                                                                                       26-OCT-1998;
                                                                                                                                                                                                                                                                                                       23-OCT-1998;
                                                                                                                                                                                                                                                                                                                     24-OCT-1997;
                                                                                                                                                                                                              WO9921977-A1
                                                                                                                                                                                                                                            06-MAY-1999.
                                                                                                                                                                                                                                                                                                                                                                                Brasch MA,
                                                                                                                                                                                  Synthetic
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                                                            AAX78977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
RESULT 23
AAX78977
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AAT48210-25 are att recombination site core region DNA sequences. The core region has at least one engineered mutation that enhances recombination in the formation of a Cointegrate or Product DNA. These core regions can be incorporated into novel vector donor DNA molecules. The nucleic acids, vectors and methods of the invention are engineered recombination sites in vitro or in vivo. The improved specificity, speed and yields of the invention facilitates DNA or RNA subcloning, regulation or exchange useful for any related purpose, e.g. in vitro recombination of DNA segments, and in vitro or in vivo insertion or modification of transcribed, replicated, isolated or genomic DNA or modification of transcribed, replicated, isolated or genomic DNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                 Nucleic acids, vectors and methods to obtain chimeric nucleic acid using recombinant proteins and engineered recombination sites in vitro or in vivo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide #16 for recombination and cloning method.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cloning; donor; recombination site; vector; chimeric; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23.4; DB 18;
Pred. No. 1.2;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 5 A; 4 C; 6 G; 10 T; 0 other;
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                                                                                                                                                                                                                                                                            Claim 14; Page 56; 106pp; English.
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                                                                                                                                   LIFE-) LIFE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 93.6%;
1 Similarity 96.0%;
24; Conservative 0
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97US-0065930.
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                                                                                                           95US-0486139.
                                                                               96WO-US10082.
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                                                                                                                                                                 Hartley JL;
                                                                                                                                                                                          WPI; 1997-065168/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09921977-A1
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                                                                               07-JUN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brasch MA,
                                                                                                                                                                  Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX78950;
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us-10-055-001a-10.rng

Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds.

Acceptor vector pHELLSGATE nuclectide sequence SEQ ID NO:13.

(first entry)

11-DEC-2002

ABQ82130;

ABQ82130 standard; DNA; 18691 BP.

RESULT 22 ABQ82130/

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New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.
                                                                                                                                  Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 25; DB 24; Length 18691; 100.0%; Pred. No. 0.43; ive 0; Mismatches 0; Indels 0;
                                                                                                                 Acceptor vector pHELLSGATE nucleotide sequence SEQ ID NO:13.
GITCAGCITITITIGIACAAGITGG 5482
                                                                                                                                                                                                                                                                                    (CSIR ) COMMONWEALTH SCI & IND RES ORG.
                                                                                                                                                                                                                                                                                                         Wesley S, Waterhouse P, Helliwell C;
                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13; Page 62-72; 104pp; English
                                                   ABQ82130 standard; DNA; 18691 BP
                                                                                                                                                                                                                                                     26-JAN-2001; 2001US-264067P.
29-NOV-2001; 2001US-333743P.
                                                                                                                                                                                                                                  24-JAN-2002; 2002WO-AU00073
                                                                                            11-DEC-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          phenotypic expression
                                                                                                                                                                                                                                                                                                                             WPI; 2002-682669/73.
                                                                                                                                                                                         WO200259294-A1
                                                                                                                                                                    Synthetic.
5458
                                                                        ABQ82130;
                             RESULT 21
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New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.

Claim 13; Page 62-72; 104pp; English.

(CSIR ) COMMONWEALTH SCI & IND RES ORG.

24-JAN-2002; 2002WO-AU00073. 26-JAN-2001; 2001US-264067P. 29-NOV-2001; 2001US-333743P.

WO200259294-A1.

Synthetic.

01-AUG-2002.

Waterhouse P, Helliwell C;

Wesley S,

WPI; 2002-682669/73.

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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (I) promoter or promoter region capable of being recognized by RNA polymerases of a cukaryotic cell or by prokaryotic RNA polymerases (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, (iii) 3' transcription termination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites, do not recombine with each the third and fourth recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for allending target nucleic acid sequences. The vectors can also be used to convent a DNA fragment tinto an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to polyade more plants with the same conventions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ion of nucleic acids. The present sequence represents nucleotide sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 other;
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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a ceipient cell, preferably in bacteria such as Escherichia coli; (b) selectable marker region capable of being expressed in the recipient cell, and (c) a chimeric DNA construct comprising: (i) promoter or cell, and (c) a chimeric DNA construct comprising: (i) promoter of promoter region capable of being recognized by RNA polymerases of a cukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyademylation region functional in the eukaryotic cell. The first can fourth recombination sites; (iii) 3' transcription termination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination site, and other or with a same recombination sites, do not recombine with each other or with a same recombination sites, do not recombine with each other or with a same recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used to solver in DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a conventional breeding scheme to produce more plants with the same convention of the con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              phenotypic expression of nucleic acids. The present sequence represents an acceptor vector nucleotide sequence from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18691 BP; 4837 A; 4621 C; 4607 G; 4626 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GITCAGCITITITIGIACAAGIIGG 25
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Les 25; Conservative
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Gaps

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17792 GTTCAGCTTTTTTGTACAAGTTGG 17816

1 GTTCAGCTTTTTTGTACAAGTTGG 25

Local Similarity 100.

Best Loca Matches

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Query Match

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The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, and attB2 mulecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination sites and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising a second recombination site and a second mucleic acid molecule comprising a second recombination site that interacts with the mutated comprising a second recombination site that interacts with the mutated comprising a second recombination site that interacts and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
              regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (1), (II), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         attB2, attP1, auseful for the
                                                                                                                                                                                                               ô
                                                                                                                                                                       100.0%; Score 25; DB 21; Length 5156; 100.0%; Pred. No. 0.38;
  operably linking nucleic acid molecules of
                                                                                                                                  Sequence 5156 BP; 1413 A; 1183 C; 1216 G; 1342 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated nucleic acid molecules encoding an attBl, attLl, attL2, attRl, and attR2 nucleotide sequence recombinational cloning of polypeptides -
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                                                                                                                                                                                 100.0%; Pred. w..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Donor plasmid pDONR207 nucleotide sequence.
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                                                                                                                                                                                                                                                                                      212 GrickGerririrgiacaaagirgg 236
                                                                                                                                                                                                                                                 TITGIACAAAGIIGG 25
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                                                                                                                                                                                                                                                                                                                                                                                  AAC55632 standard; DNA; 5584
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99US-0136744.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                         Best_Local Similarity 100.
Matches 25; Conservative
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                                                                                                                                                                                                                                                 1 GTTCAGCTTT
  desired proteins,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
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                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the secon population of nucleic acid with a second target nucleic acid -
proteins, operably linking nucleic acid molecules of interest
            regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (1), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              recombination; nucleic acid selection; ds.
                                                                                                                                                       100.0%; Score 25; DB 21; Length 5584; 100.0%; Pred. No. 0.39;
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                                                                                                                      Sequence 5584 BP; 1521 A; 1294 C; 1341 G; 1428 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       represents the donor plasmid pDONR207 nucleotide sequence.
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                                                                                                                                                                                                                            1 GTICAGCITITITIGIACAAAGIIGG 25
                                                                                                                                                                                                                                                   5458 GTTCAGCTTTTTTGTACAAAGTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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                                                                                                                                                                                         25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acid insertion;
nucleic acid isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cheo D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-129436/12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
ses 25; Conserva
                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200295055-A2
                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                 ABZ58766;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                       Query Match
desired
                                                                                                                                                                           Local
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                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                              RESULT 20
                                                                                                                                                                                                                                                                                                                              ABZ58766
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1 GTTCAGCTTTTTGTACAAGTTGG 25

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The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attL1, attL2, attB1, attB2 chocoding an attB1 attB2, attB1, attB2, attL1, attL2, attB1, and attB2 chocitde sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination sites and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising a second recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from
                                                                                                                                                                                                                                                                                                                                                                                                                   ö
of nucleic acid with a second target nucleic acid; and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. The present sequence represents the destination plasmid pDONR201 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   attP2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage lambda; att; recombination site; attB; attP; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1 and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                      DB 25; Length 4470; 0.38; 0; Indels 0
                                                                                                                                                                                                                                                                 Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cheo D;
                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Donor plasmid pDONR205 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                          Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 GTTCAGCTTTTTTGTACAAAGTTGG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 GTTCAGCTTTTTGTACAAGTTGG 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Fig 53; 459pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC55525/c
ID AAC55525 standard; DNA; 4939 BP.
                                                                                                                                                                                                                                                                                                                                  ch 100.0%;
1 Similarity 100.0%;
25; Conservative 0
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99US-0126049.
99US-0136744.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-543948/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAC55525;
                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 8
                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attB1, attB2, attB1, and attR2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        attB2, attP1, attP2, useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
desired proteins, operably linking nucleic acid molecules of interest regulatory genetic sequences, constructing genes for fusion proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the
                                    changing copy number, changing replicons, cioning into phages and cloning: (1), (II), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                  0
                                                                                                                                                                         100.0%; Score 25; DB 21; Length 4939; 100.0%; Pred. No. 0.38; O; Mismatches 0; Indels 0;
                                                                                                                                    Sequence 4939 BP; 1193 A; 1285 C; 1152 G; 1309 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acid molecules encoding an attBl, attLl, attL2, attRl, and attR2 nucleotide sequence recombinational cloning of polypeptides -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Donor plasmid pDONR206 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheo
                                                                                                                                                                                                                                                                                              3661 Gricagcriririrgracaaagrigg 3637
                                                                                                                                                                                                                                                         25
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                                                                                                                                                                                                                                                         1 GTTCAGCTTTTTTGTACAAGTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 9; Fig 54; 459pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0122389.
99US-0126049.
99US-0136744.
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                                                                                                                                                                                                                                                                                                                                                                                              AAC55526 standard; DNA; 5156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-MAR-2000; 2000WO-US05432.
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                                                                                                                                                                                              Local Similarity 100.
nes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-543948/49.
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23-MAR-1999;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-SEP-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC55526;
                                                                                                                                                                             Query Match
                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                     RESULT 18
                                                                                                                                                                                                                                                                                                                                                                           AAC55526
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Fri Nov

molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site and a second att recombination site and a second att comprising at comprising one or more mutated att recombination sites comprising at comprising one or more mutated att recombination site and a second mucleic acid molecule (III) recombination between a first mucleic acid molecule comprising a second recombination site and a second mucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site und a second mucleic acid molecule of att recombination site used for the recombinational cloning of rom the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (III), her present sequence is production of polypeptides and antibodies. The present sequence is ch 100.0%; Score 25; DB 21; Length 4208; Similarity 100.0%; Pred. No. 0.38; 25; Conservative 0; Mismatches 0; Indels 0. Sequence 4208 BP; 1172 A; 997 C; 875 G; 1164 T; 0 other; used in the exemplification of the present invention. 1 GITCAGCITITITIGIACAAAGIIGG 25 Query Match Best Local Similarity AAC55521; Matches g

Donor plasmid pDONR201 nucleotide sequence. 3283 GITCAGCITITIGIACAAAGIIGG 3259 AAC55521 standard; DNA; 4470 (first entry) 11-JAN-2001

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda Synthetic

WO200052027-A1.

08-SEP-2000

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999;

02-MAR-2000; 2000WO-US05432.

28-MAY-1999;

(LIFE-) LIFE TECHNOLOGIES INC.

WPI; 2000-543948/49

Hartley JL, Brasch MA, Temple GF,

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Cheo

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL1, attL2, attR1 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 9; Fig 49; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attR2, attR1, and attR2

mucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising the comprising a second recombination site and a second nucleic acid molecule att recombination site. (I), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of mucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, regulatory genetic sequences. changing copy number, changing replicons, cloning into phages and cloning. (1), (II), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. 99999999999999999999<del>8</del>8

Sequence 4470 BP; 1193 A; 1037 C; 977 G; 1263 T; 0 other;

Gaps 0 100.0%; Score 25; DB 21; Length 4470; 100.0%; Pred. No. 0.38; 0; Indels 0.38; 0; Mismatches 25; Conservative Similarity Query Match Best Local S Matches

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ò g

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Gaps

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RESULT 16

ABZ58767 standard; DNA; 4470 BP. ABZ58767/c ID ABZ58

ABZ58767; 

01-MAY-2003 (first entry)

Destination plasmid pDONR201 nucleotide sequence.

Nucleic acid insertion, recombination, nucleic acid selection, nucleic acid isolation, ds.

Synthetic.

WO200295055-A2.

28-NOV-2002.

21-MAY-2002; 2002WO-US15947.

21-MAY-2001; 2001US-291973P.

(INVI-) INVITROGEN CORP.

WPI; 2003-129436/12.

Brasch MA, Cheo D,

Byrd DRN;

Esposito D,

Li X,

Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid.

Disclosure, Fig 26B-C; 273pp; English.

The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid; (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of molecules to form a second population; (c) mixing the second population

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molecule (II) comprising one or more att recombination sites comprising molecule (II) comprising one or more att recombination sites comprising of interaction mitters core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated muleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising a second recombination site and a second muleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site and a second molecule comprising a second recombination site that interacts with the mutated att recombination site and second molecule comprising of the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking mucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning into the present invention.

Coloning: (III), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is
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Seguence 4165 BP; 1117 A; 926 C; 925 G; 1196 T; 1 other;

; 0 Score 25; DB 21; Length 4165; Pred. No. 0.38; 0; Indels 0; Mismatches 1 GITCAGCITITITIGIACAAAGTIGG 25 100.0%; Query Match
Best Local Similarity 100.03
Matches 25; Conservative ठे g

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Gaps

212 Gricagóriririridadadrigo 236

RESULT 13 AAC55522

AAC55522 standard; DNA; 4204 BP AAC55522; Donor plasmid pDONR202 nucleotide sequence.

11-JAN-2001 (first entry)

Bacteriophage lambda; att; recombination site; attB; attP; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda Synthetic.

WO200052027-A1.

38-SEP-2000

02-MAR-2000; 2000WO-US05432.

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999;

(LIFE-) LIFE TECHNOLOGIES INC

ä Cheo Temple GF, Brasch MA, 'n, Hartley

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 9; Fig 50; 459pp; English

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attR1, and attR2

molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination sites and (2) an isolated mucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site and a second nucleic acid molecule comprising tree treems invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion targe from essing copy number, changing replicons, cloning into phages and cloning (I) (III), ( ö Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; Also described are: (1) an isolated nucleic acid Gaps 0 Length 4204; Sequence 4204 BP; 1198 A; 912 C; 959 G; 1135 T; 0 other; mutant, recombinational cloning; entry vector; degene product targeting; fusion tag cleavage; ds. ä Donor plasmid pDONR203 nucleotide sequence. Cheo 260 GricaGCriririristacaaaGrigG 284 1 GTTCAGCTTTTTGTACAAAGTTGG 25 Brasch MA, Temple GF, (LIFE-) LIFE TECHNOLOGIES INC. 99US-0122389. 99US-0126049. 99US-0136744. AAC55523 standard; DNA; 4208 02-MAR-2000; 2000WO-US05432. Query Match
Best Local Similarity luv..
Local Similarity luv.. 11-JAN-2001 (first entry) Bacteriophage lambda WO200052027-A1. 02-MAR-1999; 23-MAR-1999; Hartley JL, 28-MAY-1999; 38-SEP-2000. Synthetic. AAC55523; RESULT 14 AAC55523/c ď à

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 9; Fig 51; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attB2, attR1, and attR2

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The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated nucleic acid molecules encoding an attBl, attBl, attLl, attLL, attLL, attLL, attLL, attLL, and attR2 nuclectide sequence useful for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   recombinational cloning of polypeptides
                                            Disclosure; Fig 13A; 273pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Fig 9; 459pp; English.
                                                                                                                                                                                                                                                                     AAC55382 standard; DNA; 233 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LIFE-) LIFE TECHNOLOGIES INC.
                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2000; 2000WO-US05432.
                                                                                                                                                                                                  25; Conservative
                                                                                                                                                                                                                                                                                                                                                               Bacteriophage lambda
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WPI; 2003-129436/12.
                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                        28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-1999;
                                                                                                                                                                                                                                                                                                   11-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                            08-SEP-2000,
                                                                                                                                                      invention
                                                                                                                                                                                                                                                                                    AAC55382;
                                                                                                                                                                                                  Matches
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nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising of interaction minits core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated mucleic acid molecule (III) comprising one or more muttad att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising a second recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site and second nucleic acid molecule of trom the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning (I), (III), (III), how cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21; Length 233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 233 BP; 73 A; 32 C; 34 G; 94 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ö,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Donor plasmid pDONR204 nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cheo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; 100.0%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GITCAGCTITITIGIACAAGIIGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Temple GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          134 Girchgerrrrrraracaagrree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC55524 standard; DNA; 4165 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0122389.
99US-0126049.
99US-0136744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-2000; 2000WO-US05432.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0
watches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-543948/49.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-MAR-1999;
23-MAR-1999;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAC55524;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                              The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first target nucleic acid molecules of nucleic acid with a second population, (c) mixing the second population of nucleic acid with a second target nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for selecting and isolating nucleic acid molecules. Sequences ABZS8727-762 represent att recombination site sequences used in the method of the
                                                                            the second
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
                                                   Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the secor population of nucleic acid with a second target nucleic acid -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.25;
-hag 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombination site nucleotide sequence attP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 27 BP; 6 A; 4 C; 6 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 25; 100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTICAGCTITITIGIACAAAGTIGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gricagcirritigiacaaagrigg 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0122389.
99US-0126049.
99US-0136744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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attP2,

attP1, a for the

Isolated nucleic acid molecules encoding an attB1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence useful recombinational cloning of polypeptides -

Example 9; Fig 52; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attL1, attR2

05-DEC-2002

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The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting chromosomes. The invention also relates to methods for targeting cinsertion of heterologous DNA into plant artificial chromosomes to selected cells and tissues. The isolated plant artificial chromosome (PAC) is useful for producing a transported plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous mucleic acid encoding a gene product such as enzymes, antisense RNA, tRNA, structural proteins, marker proteins, lagands, receptors, ribozymes, therapeutic proteins, marker biopharmaceutical proteins, rationes, or a product that provides for cesistance to disease, insects, herbicides, or stress in a plant. The heterologous nucleic acid optionally encodes a product that alters heterologous nucleic acid optionally encodes a product that alters agronomically important trait in the plant, e.g. a product that alters nutrient use and/or improves the nutrient quality of the plant. The heterologous nucleic acid is contained within a bacterial artificial chromosome (BAC) or a yeast artificial chromosome (MAC). This proved the method for a product and an oligo relating to the method for a product and a product chart alters are allowed the artificial chromosome (MAC). This
                                                                                                                                                                                                                                                                 Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteriophage lambda; recombination; att Bite; PCR primer; lambda Int;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 25; DB 25; Length 25;
Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        producing plant artificial chromosomes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
                                                                                                                                       (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTTCAGCTTTTTTGTACAAAGTTGG 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phage-lambda recombination site attPl.
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 263; 269pp; English.
                                                                                                                                                                                               Perkins E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTICAGCTITITIGIACAAGTIGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lambda integrase; therapeutic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS06179 standard; DNA; 27 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100.0%;
Matches 25; Conservative 0
                                       30-MAY-2002; 2002WO-US17451.
                                                                            30-MAY-2001; 2001US-294687P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                               Fabijanski SF,
                                                                                                                                                          (AGRI-) AGRISOMA INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteriophage lambda
                                                                                                                                                                                                                                    WPI; 2003-140436/13
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                                                                                                                                                                                               Perez C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS06179;
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11-DEC-2000; 2000WO-US33546.

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AASO6174-AASO6322 represent Bacteriophage lambda att recombination att enducies acid sequences, and PCR primers of the invention. The att sequences are recognised by the recombination protein lambda integrase (Int). The invention is a new method of producing a population of hybrid nucleic acids comprising mixing at least a first population of hybrid nucleic acids comprising mixing at least a first population of nucleic acids comprising one or more recombination sites and causing some or all of the nucleic acids to recombine with all or some of the target nucleic acids. The method is useful for producing a population of hybrid nucleic acids which may be the same or different. The nucleic may also be used to express therapeutic proteins or peptides and they may also be used to create novel fusion proteins by expressing different sequences linked to each other. The method allows simultaneous cloning of two or more different nucleic acids.
                                                                                                                                                                                             Producing hybrid nucleic acids, useful for expressing novel therapeutic polypeptides, by mixing the same or different nucleic acids having one or more recombination sites in the presence of recombination proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid insertion; recombination; nucleic acid selection; nucleic acid isolation; att; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                      Byrd DRN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 25; DB 22;
100.0%; Pred. No. 0.25;
cive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 27 BP; 6 A; 4 C; 6 G; 11 T; 0 other;
                                                                                                                                        Temple GF, Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GITCAGCITITIGIACAAAGIIGG 25
                                                                                                                                                                                                                                                                            Disclosure; Fig 24A; 357pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Att site nucleotide sequence attPl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
10-DEC-1999; 99US-0169983.
09-MAR-2000; 2000US-0188020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 100...
Thes 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-MAY-2002; 2002WO-US15947
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABZ58732 standard; DNA; 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-2003 (first entry)
                                           CHEO D.
BRASCH M A.
TEMPLE G F.
HARTLEY J L.
                                                                                                                                      Brasch MA,
                                                                                                                                                                   WPI; 2001-356174/37
                                                                                                         BYRD D R N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INVI-) INVITROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200295055-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brasch MA,
                                                                                                                                                                                                                                                e.g. Cre -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABZ58732;
                                                                                                         (BYRD/)
                                                                                                                                      Cheo D,
                                           (CHEO/)
(BRAS/)
                                                                         (TEMP/)
(HART/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
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ID ABZ5
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Chromosome-based platform; artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; PCR primer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                               Recombination site related oligonucleotide SEQ ID NO:55.
                                                                                                                                                                                                                                                                                                          100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                               1 GTTCAGCTTTTTTGTACAAGTTGG 25
                                                                                                                                                                                                                                                                                                                                      GTTCAGCTTTTTTGTACAAAGTTGG 25
                                                                                                                                                                                                                                                                                                                                                                          ACC44664 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                   29-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                   25; Conservative
                                                                              WPI; 2002-682669/73.
                                                                                                                                                                                                                                                                                                             Best Local Similarity
WO200259294-A1
            01-AUG-2002
                                                                   Wesley S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic
                                                                                                                                                                                                                                                                                                                                                                                       ACC44664;
                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                   RESULT 7
à
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The present invention describes a vector (I) comprising operably linked

The present call, preferably in bacteria such as Bacherichia coli;

(b) selectable marker region capable of being expressed in the recipient

(c) selectable marker region capable of being expressed in the recipient

CC promoter region capable of being recognized by RNA polymerases of a

cell; and (c) a chimeric DNA construct comprising; (i) promoter or

CC promoter region capable of being recognized by RNA polymerases of a

cell; and fourth recombination sites; (ii) 3' transcription terminating

and polyadenylation region functional in the ewkaryotic cell. The first

and fourth recombination sites; (iii) 3' transcription termination

CC preferably are identical. The first and second and third recombination

CC preferably are identical. The first and second recombination sites, and

CC the third and fourth recombination sites, do not recombine with each

CC ther or with a same recombination site. The vector is useful for

CC producing large amounts of double-stranded RNA which can be used to

CC convert a DNA fragment into an inverted repeat structure. Plants

CC convert a DNA fragment three present invention can be used in a

CONVENTION of the present invention and person in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        conventional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the phenotypic expression of nucleic acids. The present sequence represents the core sequence of recombination site attBl which is given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 24; Length 25; 100.0%; Pred. No. 0.25; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                   (CSIR ) COMMONWEALTH SCI & IND RES ORG.
                                                                                                                                                                                                                                                                                                                                                                      Helliwell C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 12; Page 15; 104pp; English.
24-JAN-2002; 2002WO-AU00073.
                                                                                                   26-JAN-2001; 2001US-264067P
29-NOV-2001; 2001US-333743P
                                                                                                                                                                                                                                                                                                                                                                      Waterhouse P,
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Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of

Claim 43; Page 143; 272pp; English.

interest

Leung J, Fleming E;

Lindenbaum M, Greene A,

Perez C, Li Shellard J;

Perkins E, Stewart S,

WPI; 2003-140461/13

(CHRO-) CHROMOS MOLECULAR SYSTEMS INC.

30-MAY-2002; 2002WO-US17452. 30-MAY-2001; 2001US-294758P. 21-MAR-2002; 2002US-366891P.

WO200297059-A2

05-DEC-2002.

The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (1) a platform artificial chromosome expression system (Aces) (II) comprising several sites that participate in recombinase catalysed recombination; and (2) a method (MI) for introducing a heterologous nuclaic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for introducing a heterologous nuclaic acid molecule into a platform artificial chromosome, preferably an Aces. (II) is useful for producing a transfencing (II) by cell fusion, lipid-mediated transfection by a carrier system, microaniscial into an embryonic microprojectile bombardment or direct DNA transfer into an embryonic chromosome. ö cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACes comprising random portions of a genome. ACC44612 to ACC44732 and ABP96650 to ABP96657 represent sequences used in the Plant artificial chromosome, PAC; transgenic plant; vaccine; blood factor; herbicide; stress; agronomical; nutrient quality; bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC; Gaps ö 100.0%; Score 25; DB 25; Length 25; 100.0%; Pred. No. 0.25; 0; Indels Artificial plant chromosome related oligo SEQ ID No 46. 0.25; Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other; 0; Mismatches exemplification of the present invention. 25 1 GTTCAGCTTTTTTGTACAAAGTTGG 25 1 GTTCAGCTTTTTTGTACAAGTTGG ABT16634 standard; DNA; 25 BP. (first entry) 25; Conservative Best Local Similarity 03-APR-2003 ABT16634; Query Match Matches RESULT 8 ð 셤

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Gaps ..

WO200296923-Al,

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The present invention describes an isolated nucleic acid molecule (I) comprising a first nucleic acid sequence having a defined sequence (AAC87866 to AAC87881, sequences complementary to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87881.

To are: (1) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site that removes one or more actor adons from the being an att or lox site; (2) an isolated nucleic acid molecule (III) comprising a first att recombination site omprising a mutation that enhances recombination specificity; (3) vectors (IV) comprising the above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids; and (4) cells comprising the above mutative sites suitable for subcloning reactions. The use of nucleic acids or (IV). The nucleic acids are used in engineering a core region of a given recombination site to provide mutative sites suitable for subcloning reactions. The use of nucleic acids and the methods for DNA or RNA subcloning, highly specific, rapid, and less labour intensive.
                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank a selectable marker and comprise a core region having an engineered
                 Core region, recombination site, cloning, chimeric DNA, characteristic, mutation, att site, lox site, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Column 18; 73pp; English.
                                                                                                                                                                                                                                                                (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABQ82127 standard; DNA; 25 BP
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                                                                                                                                                                                                                                                                                               Brasch MA, Hartley JL;
                                                                                                                                                                                                                                                                                                                                WPI; 2001-049004/06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                               Sscherichia coli
                                                                                                                                                                20-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors each comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture; and selecting for a host comprising the chimeric nucleic acid molecule, and selecting for a host comprising the vectors comprising the second vector; to clone the nucleic acid. The present sequence is a recombinantion site, which may be used in the method of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Escherichia coli core region recombinant site attP1 SEQ ID NO:15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
 25
                  GTTCAGCTTTTTTGTACAAAGTTGG 25
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GTTCAGCTTTTTGTACAAAGTTGG
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                                                                                                                                                                                                                                               Recombination site; cloning; att;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (LIFE-) LIFE TECHNOLOGIES INC
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95US-0486139.
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                                                                                                               AAF55749 standard; DNA; 25
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                                                                                                                                                                             (first entry)
                                                                                                                                                                                                              Recombination site attP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brasch MA;
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                                                                                                                                                                                                                                                                                                                                                                            12-JAN-1998;
                                                                                                                                                                                                                                                                              Unidentified
                                                                                                                                                                                                                                                                                                             JS6171861-B1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention.
                                                                                                                                              AAF55749;
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                                                                               RESULT 4
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0
                                                        Length 25;
                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Core sequence of recombination site attP1 SEQ ID NO:10.
                                               th 100.0%; Score 25; DB 22; Similarity 100.0%; Pred. No. 0.25; 25; Conservative 0; Mismatches 0;
Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
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The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NAMS) comprising: (a) combining in vitro or in vivo: (1) at least one insert donor molecules (IDMS) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMS) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or sites specific recombination proteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the VDMs, thereby producing one or more desired product molecules (PMS). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that
                                                                  AAT48210-25 are att recombination site core region DNA sequences. The recombination in the formation of a Cointegrate or Product DNA. These core regions can be incorporated into novel vector donor DNA molecules. The nucleic acids, vectors and methods of the invention are used to obtain chimeric nucleic acid using recombination proteins and engineered recombination sites in vitro or in vivo. The improved specificity, speed and yields of the invention facilitates DNA or RNA subcloning, regulation or exchange useful for any related purpose, e.g. in vitro recombination of DNA segments, and in vitro or in vivo insertion or modification of transcribed, replicated, isolated or genomic DNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cloning; donor; recombination site; vector; chimeric; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oligonuclectide #15 for recombination and cloning method
                                                                                                                                                                                                                                                                                                                  Seguence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                              1 GITCAGCTITITIGIACAAGITGG 25
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                                   Claim 14; Page 56; 106pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acid cloning methods
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                                                                                                                                                                                                                                                                                                                                                                                          25; Conservative
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                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
 vitro or in vivo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-OCT-1998;
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(first entry)

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Gaps

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100.0%; Score 25; DB 18; Length 25; 100.0%; Pred. No. 0.25; ive 0; Mismatches 0; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Methods for apposing nucleic acids comprising an expression signal and a gene/partial gene, using recombinatorial cloning by incubating the nucleic acids in the presence of a recombination protein under
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                                                                                                                                                   Gaps
have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Recombination site; copy number; replicon; recombinatorial cloning;
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                                                                                                            100.0%; Score 25; DB 20; Length 25; 100.0%; Pred. No. 0.25;
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                                                                         Sequence 25 BP; 5 A; 3 C; 6 G; 11 T; 0 other;
                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                          GTTCAGCTTTTTTGTACAAAGTTGG 25
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                                                                                                                    100.08; Fig.
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95US-0486139.
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                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-488248/53.
                                                                                                                                 Best Local Similarity
Matches 25; Conserv
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                                                                                                                                                                                                                                                                                 RESULT 3
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Temple GF;

Hartley JL,

Fox DK,

98US-0177387. 97US-0065930. 98WO-US22589.

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Acceptor vector ph Acceptor vector ph Oligonucleotide #4 attP2,P3 core regi Oligonucleotide #1 Recombination site Recombination site

Scoring table:

Total number

Searched:

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Att site nucleotid Recombination site Donor plasmid pDON

Phage-lambda recom

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att recombination site; core region; mutation; enhance; recombination; vector; subcloning; regulation; exchange; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids, vectors and methods to obtain chimeric nucleic acid - using recombinant proteins and engineered recombination sites in
                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                   ABQ82123
ABQ82128
ACC44660
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AAX78950
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AAD14444
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AAC87876
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AAC55383
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 AAT48224 standard; DNA; 25
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27
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Core sequence of r
Recombination site
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Oligonucleotide #1
                                                                           ; Search time 111.5 Seconds
(without alignments)
605.255 Million cell updates/sec
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1. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1980.DAT:*

2. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1981.DAT:*

3. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1983.DAT:*

4. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1983.DAT:*

5. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1983.DAT:*

7. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1985.DAT:*

7. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1987.DAT:*

8. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1987.DAT:*

9. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1987.DAT:*

11. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1987.DAT:*

12. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1987.DAT:*

13. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1997.DAT:*

14. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1997.DAT:*

15. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1997.DAT:*

16. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1997.DAT:*

17. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1995.DAT:*

18. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1995.DAT:*

19. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

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22. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

23. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

24. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

25. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

26. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

27. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

28. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

29. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

21. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

22. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

23. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

24. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

25. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

26. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

27. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*

28. /SIDS1/gcgdata/geneseq/genesegn-embl/NA1999.DAT:*
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           GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                      of hits satisfying chosen parameters:
                                                                                                                                                                                                  2552756 segs, 1349719017 residues
                                                                                                                                             1 gttcagcttttttgtacaaagttgg 25
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                                                                             2003, 21:05:38
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AAF55749
AAC87880
ABO82127
ACC44664
ABT16634
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AAX78949
                                                      nucleic search, using sw model
                                                                                                                                                                 IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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25
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Maximum DB seg length: 2000000000
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Result No. us-10-055-001a-10.rge

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FEATURES
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AUTHORS
TITLE
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I13139
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PD 15-JAN-2002
PF 26-OCT-1998 JP 2000518069
PR 24-OCT-1999 US 60/065930,23-OCT-1998 US 09/177387 PI
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH,GARY F TEMPLE, DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source 1.25
PT /Organism='Unknown'.
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unclassified.

Unclassified.

I (bases 1 to 201)

Okano, K. and Kambara, H.
Polynucleotide capturing support for capturing, eluting and collecting polynucleotides in a sample solution
Patent: US S81:506-A 18 06-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic construct
artificial sequences.
1 (bases 1 to 201)
Okano, K. and Kanbara, H.
CHIP FOR CATCHING POLYNUCLEOTIDE
Patent: UP 1993236997-A 11 17-SEP-1993;
HITACHI LTD
OS Artificial gene
OC Artificial sequence; Genes.
                                                                                                             /organism='Unknown'
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Seguence 18 from patent US 5817506.
AR044609
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Best Local Similarity 92.0%;
Matches 23; Conservative
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JP 1993236997-A/11.
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E05439
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AR044609
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. (bases 1 to 201)
Okano, K. and Kambara, H.
Separation of polynucleotides using supports having a plurality of
Selectrode-containing cells
Patent: US 5434049-A 18 18-JUL-1995;
Location/Qualifiers
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87.2%; Score 21.8; DB 6; Length 201;
Best Local Similarity 92.0%; Pred. No. 1.38+02;
Matches 23; Conservative 0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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92.0%; Pred. No. 1.3e+02;
tive 0; Mismatches 2;
                                                                                                                                           1. .201
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201 bp | Sequence 18 from patent US 5434049.
JP 1993236997-A/11
17-SEP-1993
28-FEB-1992 JP 1992042829
OKANO KAZUNOBU, KANBARA HIDEKI
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. 38 c 27 g
                                                                                                             topology: Linear.
Location/Qualifiers
                                                                       C12Q1/68;
strandedness: Single;
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Best Local Similarity 92.0
Matches 23; Conservative
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Job time : 602 secs
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AUTHORS JOURNAL

TITLE

FEATURES

BASE CC ORIGIN

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9805. .10110
| hote="ccdB" | codon grart=1 |
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| protein_id="AAN76305.1" |
| protein_id="AAN76305.1" |
| protein_id="G1:22988999" |
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LKTVKKNKHKEYPAPIHIIARIAMAHPBFRMAMKOGELVIMOSVHPCYTVFHBOTETF
SSIMSEYHDDFRQFIHIYSQDVACYGBNLAYFPKGFIENMFFVSANPWVSFTSFDLNV
ANMDNFFAPVFIMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
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Recombinational cloning using nucleic acids having recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translation="MEKKITGYTTVDISQWHRKEHFEAFQSVAQCTYNQTVQLDITAF
                                                                                                                                                                                                                                                                                                                                                  430. .8554
note="attR1; Gateway; Bacteriophage Lambda recombination
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/note="attR2; Gateway; Bacteriophage Lambda recombination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10419. .13990
/note="his-3 right flank; his-3 target integration site"
3549 c 3559 g 3497 t
Replacement Plasmids
Unpublished
1 (bases 1 to 13990)
Haag.J.R., Lee,D.W. and Aramayo,R.
Direct Submission
Submitted (27-AUG-2002) Biology, Texas A&M University, BSBW #415,
College Station, TX 77843-3258, USA
Location, Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    unidentified
unclassified.
1 (bases 1 to 25)
Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.
Recombinational cloning using nucleic acids having recombination
Datent: JP 2002500861-A 42 15-JAN-2002;
LIFF TECHNOLOGIES INC
OS Unknown
PN JP 2002500861-A/42
                                                                                                                                                                                                                                                                                                                       note="his-3 left flank; his-3 target integration site"
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                                                                                                                                                                        /organism="his-3 integration vector pJHAM007"
/mol type="genomic DNA"
/specific_host="Neurospora crassa"
/db_xref="taxon:211505"
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Pred. No. 32;
0; Mismatches
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Matches 23; Conserv
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                                                                 Goossens, A. and Inz, D. The use of genes encoding membrane transporter pumps to stimulate the use of genes encoding membrane in biological cells patent: WO 02083888-A 9 24-OCT-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE) Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          his-3 integration vector pJHAM007
his-3 integration vector pJHAM007
artificial sequences; vectors.
1 (bases 1 to 13990)
Haag,J.R., Lee,D.W. and Aramayo,R.
Description of a GATEWRY Destination Vector For High-Throughput
Construction of Neurospora crassa Histidine-3 (his-3)-Gene
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89.6%; Score 22.4; DB 6; Length 13274;
Best Local Similarity 95.8%; Pred. No. 32;
Matches 23; Conservative 0; Mismatches 1; Indels 0;
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Syngenta Participations AG (CH); Universitaet Zuerich
Location/Qualifiers
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89.6%; Score 22.4; DB
Best Local Similarity 95.8%; Pred. No. 33;
Matches 23; Conservative 0; Mismatches
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Sequence 20 from Patent WO0206490.
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/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/db_xref="taxon:32630"
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/note="SV40"
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PiggyBac transformation vector pB-UGIR w+, complete seguence.
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1 (bases 1 to 12677)

Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, B.P. A toolkit for transformation and mutagenesis in Drosophila using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Spana, E.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         piggyBac
Unpublished
2 (bases 1 to 12677)
Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P
Direct Submission
Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park,
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/note="Gateway recombination cassette A; attR1 CmR ccdB
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    Abb_xref="taxon:221642"

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Pred. No. 33;
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complement (c9370. 9819)
/transposon(="piggyBac transposable element"
a 2924 c 2833 g 3497 t
                                                   /note="8240"
3574. 7697
/gene="win'-white; derived from Drosophila"
complement(<7698. .8147)
/transposon="piggyBac transposable element"
a 2528 c 2491 g 3034 t
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/note="SV40"
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/note="RpS5"
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piggyBac transformation vector pB-UGIR w+
artificial sequences; vectors.
1 (asses 1 to 126/7), Andersen,R.O., Stam,L.F. and Spana,E.P.
Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
A toolkit for transformation and mutagenesis in Drosophila using
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/organism="piggyBac transformation vector pB-UGIR/Organism="piggyBac transformation vector pB-UGIR/Mol_type=genomic DNA"
/db xrefe="texon:221642"
complement(11. .>620)
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/gene="w"
/note="win:white; derived from Drosophila"
complement(<9370. .9819)
/transposon="piggyBac transposable element"
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/note="5x UAS hsp70 TATA signal"
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Pred. No. 33;
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Sequence 9 from Patent W002083888.
AX590202
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VERSION
KEYWORDS
SOURCE
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gene

gene

CDS

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circular SYN 26-FEB-2003 w+, complete sequence.
                                                                                                                 1. .11005 Page Page Transformation vector pB-UGateway w+" /mol_type="genomic DNA" /db xref="taxon:221641" complement(11. .>620)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      piggyBac transformation vector pB-UGateway w+
piggyBac transformation vector pB-UGateway w+
artificial sequences; vectors.
1 (bases 1 to 11005)
Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
A toolkit for transformation and mutagenesis in Drosophila using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              piggyBac
Unpublished
2 (bases 1 to 11005)
Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, B.P.

    .11005
/organism="piggyBac transformation vector pB-UGateway w+"

2 (bases 1 to 11005)
Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
Direct Submission
Submitsed (13-DBC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, N 27709, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    643. .999
/note="5x UAS hsp70 TATA signal"
1003. .2713
/note="Gateway recombination cassette A; attR1 CmR ccdB
                                                                                                                                                                                                                                                                                                      1003. .2713
/note="Gateway recombination cassette A; attR1 CmR ccdB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (13-DEC-2002) Invertebrate Targets, Syngenta Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 11005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="w"
/note="mini-white; derived from Drosophila"
complement(<7698. .8147)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /transposon="piggyBac transposable element"
2528 c 2491 g 3034 t
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/transposon="piggyBac transposable
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AX196824.1 GI:28565716
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Pred. No. 34;
0; Mismatches
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/note="5x UAS hsp70 TATA
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/db_xref="taxon:221641"
complement(11..>620)
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note="RpS5"
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                                                                                                                                                                                                                                                                                                                                                                                           /gene="ccdB" /note="encodes a cytotoxic protein that is a potent poison of DNA gyrase"
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SSLMSEYHDDFRQFIHIYSQDVACYGENLAYFPKGFIENMFFVSANPWVSFTSFDLNV
ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MOFKVYTYKRESRYRLFVDVQSDIIDTPGRRMVIPLASARLLSD
KVSRELYPVVHIGDESWRMMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
complement (2008). .3547)
                                                                                /translation="MOFKVYTYKRESRYRLFVDVQSDIIDTPGRRMVIPLASARLLSD
KVSRELYPVVHIGDESWRMMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
                                                                                                                                                                                                                                                                  gene and
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piggyBac transformation vector pB-UGateway w+
artificial sequences; vectors.

1 (bases 1 to 11005)
Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, E.P.
A toolkit for transformation and mutagenesis in Drosophila using biggyBac
Unpublished
                                                                                                                                                                1762. .2048
/note="contains intron 1 of Arabidopsis thaliana WRKY transcription factor 33"
complement (2073. .3783)
/note="anisense orientation of Gateway conversion cassette frame A containing attR1-R2 repeats, CMR gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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/note="attR1 of Gateway conversion cassette frame A"
2150 c 2185 g 2347 t
                                                                                                                              1610. .1736
/note="attR2 of Gateway conversion cassette frame A"
                                                                                                                                                                                                                                                                                                                             conversion cassette frame A"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="CmR"
/function="confers resistance to antibiotic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="CcdB"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAM62302.1"
/db_xref="GI:21552739"
                         product="CcdB"
protein_id="AAM62301.1"
                                                                                                                                                                                                                                                                                                                           /note="attR2 of Gateway complement(2241. .2546)
                                                                                                                                                                                                                                                                                                          .2199)
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                                                               db xref="GI:21552738"
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complement (2073.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
/product="CmR"
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Matches 23;
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BASE COUNT

ORGANISM

KEYWORDS

RESULT 30

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AY196824 LOCUS

AUTHORS TITLE

JOURNAL

REFERENCE

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Gaps

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/protein_id="Aam62300.1"
/db_xref="G1:21552737"
/translation="WEKKITGYTTUDISQWHRKEHFEAFQSVAQCTYNQTVQLDITAF
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ANMDNFFAPVFIMGKYYTQGDKVLMPLAIQVHAVCDGFHVGRMLNELQQYCDEWQGG
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                                                                                                                                                                                                                                                                                                                                                     circular SYN 25-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 9019)
Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.
Direct Submission
Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
f. Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conversion cassette, CmR gene and ccdB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="binary plant gene silencing vector for one-step
cloning of inverted sequences"
3803. .9019
                                                                                                                                                         Gaps
complement(3657. .3783)
/note="attR1 of Gateway conversion cassette frame A"
1 2150 c 2185 g 2347 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26. .152
/note="attRl of Gateway conversion cassette frame
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.B. pJawohl8-RNAi a binary vector for gene silencing in plants Unpublished
                                                                                                                                                       0
                                                                                                             Length 9019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      function="confers resistance to antibiotic
                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Binary vector pJawohl8-RNAi"
/mol_type="genomic DNA"
/db_xref="taxon:188084"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Binary vector pJawohl3-RNAi"
|mol_type="genomic DNA"
|db_xref="taxon:176105"
                                                                                                                                                                                                                                                                                                                                                     AF408413 9019 bp DNA circ
Binary vector pJawohl8-RNAi, complete sequence.
AF408413
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repeats,
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/note="sense orientation of frame A containing attR1-R2
                                                                                                                                                           0; Mismatches
                                                                                                             Score 22.4; I
Pred. No. 35;
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Binary vector pJawohl8-RNAi
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1263. .1568
                                                                                                               89.6%;
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/gene="CmR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codom_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1762. .2048
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                                                                     /note="sense orientation of Gateway conversion cassette
frame A containing attRl-R2 repeats, CmR gene and ccdB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1610 .1736
/hote="attR2 of Gateway conversion cassette frame A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>-</u>
Α,
                                                                                                                                                              note="attR1 of Gateway conversion cassette frame A"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ccdB gene"
complement(2073. .2199)
note="attR2 of Gateway conversion cassette frame
complement(2241. .2546)
/gene="ccdB"
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                                                                                                                                                                                                                                                      gene="CmR"
function="confers resistance to antibiotic
                                                                                                                                                                                                                                                                                                                                                               1d="AAM62300.1"
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/gene="CmR"
                                                   .1733
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gene

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Length 4462;

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DB 12;
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     Score 22.4; DE Pred. No. 40; 0; Mismatches
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Patent: WO 0188121-A 10 22-NOV-2001;
Devgen NV (BE)
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                                                                                                                                                                                                Sequence 10 from Patent W00188121.

    .5148
    /organism="synthetic co
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Binary vector pJawohl8-RNAi
artificial sequences; vectors.
1 (bases 1 to 9019)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="Plasmid pGN39"
1199 c 1279 g
                                                                                                     480 GTTCAGCTTTTTTGTACAAACTTG 457
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                                                                              1 GITCAGCITITITITIONAAGITG 24
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     89.68;
                                                                                                                                                                                                                                                                                                synthetic construct
synthetic construct
artificial sequences.
         Query Match
Best Local Similarity 95.8<sup>1</sup>
Matches 23; Conservative
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AX306327/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Jakoby, M.J., Heim, M.A. and Weisshaar, B.
Use of a gateway compatible vector for transient plant transfection
Unpublished
                                                                                                                                                                                                                         Jakoby, N.J.
Jakoby, N.J.
Direct Submission
Submitted (26-MAR-2003) Jakoby M.J., Salamini, MPI for Plant
Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, GERMANY
Location/Qualifiers
                                 AJ551314.1 GI:29335742
amp gene; beta lactamaee; cat gene; ccdB gene; chloramphenicol
acetyl transferase; control of cell death B protein.
Transfection vector pBTdest
Transfection vector pBTdest
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 Transfection vector pBTdest
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/note="358"
456, .580
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1690. .1995
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'note="35S"
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f.Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
Germany
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="binary plant gene silencing vector for one-step cloning of inverted sequences" 3803. .9019
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Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.
Direct Submission
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Indels
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RESULT 22
AX498619
LOCUS
DEFINITION
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KEYWORDS

SOURCE ORGANISM

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

BASE COUNT ORIGIN

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circular SYN 27-MAR-2003
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                                                                                                 PAT 29-MAR-2003
                                                                                                                                                                                Escherichia coli
Escherichia coli
Bacteria, Proteobacteria, Gammaproteobacteria, Enterobacteriales,
Enterobacteriaceae, Escherichia.
                                                                                                                                                                                                                                                                        Holtzman,D., Madden,K., Maxon,M. and Sherman,A.
Modulation of secondary metabolite production by zinc binuclear
cluster proteins
Patent: WO 0224865-A 9 28-MAR-2002;
Microbia, INC. (US)
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Best Local Similarity 95.8%; Pred. No. 1.1e+02;
Matches 23; Conservative 0; Mismatches 1; Indels
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Procaryotic libraries and uses
Batent: W0 02066653-A 63 29-AUG-2002;
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ilarity 95.8%; Pred. No. 48;
Conservative 0; Mismatches
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                                                                                                 Sequence 9 from Patent WO0224865.
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DEFINITION
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Recombinational cloning using nucleic acids having recombination
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                                                          PAT 26-SEP-2002
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1 (bases 1 to 25)

HartLey, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.

HartLey, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.

Paccombinational cloning using nucleic acids having recombination

Patent: JP 2002500861-A 9 15-JAN-2002,

LIFE TECHNOLOGIES INC
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PN 197 2002500861-A/9

PD 15-JAN-2002

PP 26-OCT-1994 US 00/0518069

PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
012N15/09,C12Q1/68,C12N15/00

CC Description of Unknown Organism: recombination products FH

Key Location/Qualifiers
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Recombinational cloning using engineered recombination sites
Patent: BP 1229113-A 907-AUG-2002;
INVITROGEN CORPORATION (US)
Location/Qualifiers
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95.8%; Pred. No. 1.1e+02;
tive 0; Mismatches 1;
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Location/Qualifiers
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
/ab_xref="taxon:32644"
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Sequence 9 from Patent EP1229113.
AX498619
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BD131335.1 GI:23226280
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Best Local Similarity 95.8
Matches 23; Conservative
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KEYWORDS

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BASE COUNT ORIGIN

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Recombinational cloning using engineered recombination sites
Patent: EP 12271477.49 31.7UL-2002;
INVITROGEN CORPORATION (US)
Location/Qualifiers
                                                                            Gaps
                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: US 6270969-A 9 07-AUG-2001;
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Pred. No. 1.1e+02;
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                                                    Score 22.4; DB 6;
Pred. No. 1.1e+02;
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    /organism="unidentified"

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Sequence 9 from patent US 6270969.
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Sequence 9 from Patent EP1227147.
AX491648
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4 c 4 g
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/organism="unknown"
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Best Local Similarity 95.8
Matches 23; Conservative
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Best Local Similarity 95.8
Matches 23; Conservative
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Recombinational cloning using nucleic acids having recombination
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Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
Recombinational cloning using nucleic acids having recombination
Patent: JP 2002500861-A 16 15-JAN-2002;
LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                           OS Unknown
PN JP 2002500861-A/16
PD 15-J04-2002
PP 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
JAMES L HARLIELY MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09,C12Q1/68,C12N15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source | L. 25
FT | /organism='Unknown'.
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Hartley, J.L. and Brasch, M.A.
Recombinational cloning using engineered recombination sites
Patent: 18 6171861.A. 9 09-UAN-2001;
Location/Qualifiers
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/organism='Unknown'.
Location/Qualifiers
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96.0%; Pred. No. 43;
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Sequence 9 from patent US 6171861.
AR124529
AR124529.1 GI:14109890
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BD131342.1 GI:23226287
JP 2002500861-A/16.
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TITLE
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BD131342
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TITLE

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Hartley,J.L. and Brasch,M.A.
Recombinational clouing using engineered recombination sites
Patent: EP 1229113-A 11 07-AUG-2002;
INVITROGRAM CORPORATION (US)
Location/Qualifiers
                     Recombinational cloning using engineered recombination sites
Patent: EP 122747-A 16 31-JUL-2002;
INVITROGEN CORPORATION (US)
Location/Qualifiers
1. 25
/organism="unidentified"
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Recombinational cloning using engine
Patent: EP 1229113-A 16 07-AUG-2002;
INVITROGEN CORPORATION (US)
                                                                                                                                                                                    Score 23.4; D
Pred. No. 43;
0; Mismatches
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Sequence 11 from Patent BP1229113.
AX498621
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Sequence 16 from Patent EP1229113
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/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Hartley, J.L. and Brasch, M.A.
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                                                                                                                   Vile, R.G., Harrington, K., Murphy, S. and Bateman, A. Compositions and methods for tissue specific gene regulation
                                                                                                                                             therapy
Patent: WO 0174861-A 8 11-OCT-2001;
MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
Location/Qualifiers
1. 25
/organism="synthetic construct"
/mol_type="genomic DNA"
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/noTe="Synthetically generated vector sequence"
/noTe="Synthetically generated vector sequence"
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/organism="unidentified"
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/db_tref="taxon:32644"
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Sequence 16 from Patent EP1227147.
AX491655 AX491655.1 GI:22324163
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Sequence 11 from Patent BP1227147.
AX491650 GI:22324158
   Sequence 8 from Patent WO0174861.
AX269137
AX269137.1 GI:16542057
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Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: US 6270969-A 16 07-AUG-2001;
Location/Qualifiers
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Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engine
Patent: US 6270969-A 11 07-AUG-2001;
Location/Qualifiers
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PD 15-JAN-2002
PD 15-JAN-2002
PP 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065930, 23-OCT-1998 US 09/177387 PI
JAMES L HARTIETY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12M15/09, C12Q1/68, C12M15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT SOURCE | 1. 25
FT | FT | FT | /organism='Unknown'.
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Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: 18 6171861.A 16 09-JAN-2001;
Location/Qualifiers
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Hartley, J.L. and Brasch, M.A.
Recombinational cloning using engineered recombination sites
Patent: 18 5171861-A 11 09-JAN-2001;
Location/Qualifiers
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Pred. No. 43;
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Sequence 11 from patent US 6171861.
AR124531
AR124531.1 GI:14109892
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/organism="unidentified"
/mol_type="genomic DNa"
/db_rref="taxon:32644"
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Best Local Similarity 88.0%;
Matches 22; Conservative 3
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Query Match Best Local

Matches

source

FEATURES

REFERENCE AUTHORS TITLE JOURNAL

BASE COUNT ORIGIN

DEFINITION ACCESSION

RESULT 9 AR124531 LOCUS

SOURCE ORGANISM

VERSION KEYWORDS

DEFINITION ACCESSION VERSION KEYWORDS

RESULT 10

AR124536

SOURCE ORGANISM

source

TITLE JOURNAL FEATURES

AUTHORS

REFERENCE

ORGANISM

SOURCE

KEYWORDS

AUTHORS

REFERENCE

JOURNAL MEDLINE

TITLE

JOURNAL AUTHORS PUBMED REFERENCE

FEATURES

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Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.
Recombinational cloning using nucleic acids having recombination
Batent: 4P 2002500861-A 43 15-JAN-2002;
LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      recombination
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Recombinational cloning using nucleic acids having
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Matches 25; Conservative
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TITLE
JOURNAL
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Plant J. 27 (6), 581-590 (2001)
kanomycin resistance protein; neomycin phosphotransferase II; nptII
gene; promoter; speC gene; spectinomycin resistance protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="pHELLSGAIE is a derivative of cloning vector
pART27"
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Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualiflers
1..18691
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                                                                                        Cloning vector pHELLSGATE Cloning vector pHELLSGATE artificial sequences; vectors.
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Waterhouse, P.M.
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DLFBALNETLTLWNSPPDWAGDERNVYLTLSRIWYSAVTGKTAPKDVAADWAMBRLPA
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Best Local Similarity 100.0%; Score 25; DB 12; Length 18691;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
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                                                                                                                                                                                              note="neomycin phosphotransferase II (nptII)"
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7 g 4626 t
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/note="octopine e
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'gene="spec"
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AJ311874.1 GI:15982218
Avanomycin resistance protein; neomycin phosphotransferase II; nptII
gene; promoter; speC gene; spectinomycin resistance protein;
                                                                                                                                                                                                                                                                                                                                                                         Wesley, V.S., Helliwell, C., Smith, N.A., Wang, M.B., Rouse, D., Liu, Q., Gooding, ps., Singh, S.R., Abbott, D., Stoutjesdijk, A., Robinson, S.P., Gleave, A.P., Green, A.G. and Waterhouse, P.M. Glave, A.G. and Waterhouse, P.M. Gonstruct design for efficient, effective and high-throughput gene
                                                                                                                                               circular SYN 09-JUL-2002
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part27"
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Direct Submission
Submitted (04-My-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Camberra, ACT 2601, AUSTRALIA
Location/Qualifiers
1..18691
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| Ab_xref="taxon:358"
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449. .1442
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Plant J. 27 (6), 581-590 (2001)
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Cloning vector pHELLSGATE.
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Query Match Best Local &

Matches

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BASE COUNT ORIGIN

DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM

RESULT 2 AR163186

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TITLE JOURNAL

AUTHORS REFERENCE

BASE COUNT ORIGIN

Matches

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unidentified
unclassified.

In (Dases I. 25)

Recombinational cloning using nucleic acids having recombination
L Patent: JP 2002500861-A 15 15-JAN-2002;
LIFE TECHNOLOGIES INC
OS Unknown
Py 2002500861-A/15
Py JP 2002500861-A/15
Py JP 2002500861-A/15
Py JP 2002500861-A/15
Py JP 2002500861-A/15
Py Z-CCT-1998 US 09/177387 PI
PR 24-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI
PR 24-OCT-1997 US 60/06590,020CC
Cl2N15/09,CL2Q1/68,CL2M15/00
CC Description of Unknown Organism: recombination products FH
Key Location/Qualifiers
FT source L. Octanism: A Discount of Unknown Organism: recombination products FH
FT Source L. Octanism: A Discount of Unknown Organism: recombination products FH
FT Source L. Octanism: A Discount of Unknown Organism: Rey L. Octanism: Rey L. 
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100.0%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 9.2;
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Recombinational clouing using enginer
Patent: EP 1229113-A 15 07-AUG-2002;
INVITROGEN CORPORATION (US)
Location/Qualifiers
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Sequence 15 from Patent EP1229113.
AX498625
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JP 2002500861-A/15.
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Unclassified.
1 (bases 1 to 25)
Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: US 6270969-A 15 07-AUG-2001;
Patent: Location/Qualifiers
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Sequence 15 from patent US 6270969.
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RESULT 3
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Description	AR124535 Sequence AR463186 Sequence AX491654 Sequence AX498625 Sequence BD131341 Recombina AJ311874 Cloning v AJ311874 Cloning v AJ311874 Cloning v AJ311875 Sequence AR124531 Sequence AR124531 Sequence AR163187 Sequence AX491655 Sequence AX491655 Sequence AX491655 Sequence AX491650 Sequence	AX498619 Sequence BX013135 Recombina AX684690 Sequence AX703501 Sequence AX306327 Sequence AX408413 Binary ve AX408413 Binary ve AX408413 Binary ve AX196824 PiggyBac AX196824 PiggyBac AX196825 PiggyBac AX196826 Sequence AX56862 Sequence AX56862 Sequence AX56862 Sequence AX56862 Sequence AX56862 Sequence AX56862 Sequence BD131368 Recombina AR044609 Sequence BD13139 Sequence BJ3439 Oligonucleo I13139 Sequence BJ343 Sequence	linear PAT 16-MAY-2001
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bx400983

EX400983 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
EX400983 Home CSODK005YD11 5-PRIME, mRNA sequence.

EX400983
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315 c 336 g 239 t 28 others
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sites of the pCMVSPORT 6 vector. Library was normalized."
290 c 326 g 241 t 112 others
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                        type="mRNA"
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Clone CS0D1071YA13 5-PRIME, mRNA sequence.
                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Li, W. B., Gruber, C., Jessee, J., and Polayes, D. Full-length cDNA libraries and normalization
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BP 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 95.r For mc
information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS1A1018ZE07QP1&ccluster=95.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS1A1018ZE07QP1.
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cgi-bin/cluster.cgi?seq=CSODI085DA09NPl&cluster=9393.f. Contact
cgi-bin/cluster.cgi?seq=CSODI085DA09NPl&cluster=9393.f. Contact
Feng Liang Email : fliangelifetech.com VIX. :
Fthy/fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI085DA05NPPl.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                Contact: Genoscope Genorate Sequencage Genoscope - Centre National de Sequencage BPD 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9393.f more information about this cluster, see
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Full-length cDNA libraries and normalization
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X382731 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens CDNA
CLONE CSODI085YB18 3-PRIME, mRNA sequence.
BX382731
sites of the pCMVSPORT 6 vector. Library was normalized." 1244 c 318 g 244 t 116 others
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Li W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Inbrary was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2356.r. For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODL001DB04QP1&cluster=2356.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODL001DB04QP1.
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80.0%; Score 20; DB 13; Length 1201;
Best Local Similarity 90.9%; Pred. No. 6.5e+02;
Matches 20; Conservative 1; Mismatches 1; Indels C
                                                                                                                                                 Length 1201;
                                                                                                                              ; Score 20; DB 5; Pred. No. 6.5e+
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="CS0DL001YD08"
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/mol_type="mRNA"
/mol_type="mRNA"
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/tissue_type="NEUROBLASTOWA"
/clone lib="Homo sapiens NEUROBLASTOWA"
/clone lib="Homo sapiens"
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AL544923 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens cDNA clone CSODI012YM11 5-PRIME, mRNA sequence.
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Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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BP 191 91006 EVRY cedex - France
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7655.f For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CL0BB005ZC02FPl&cluster=7655.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CL0BB005ZC02FPl.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      On Feb 13, 2001 this sequence version replaced gi:12777665
Contact: Genoscope
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ALS44923.2 GI:31266764
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/mol type="mRNA"
/db xref="taxon:9606"
/clone="CSODIO12YM1"
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/tissue type="PLACENTA COT 25-NORMALIZED"
/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="ib="homo sapiens PlaceNTA COT 25-NORMA COT 25-NOR
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ALS54071 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA clone CSODI081YF11 5-PRIME, mRNA sequence.
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1 (Dases 1 to 1201)

Li, W.B., Gruber, C., Jessee, J., and Polayes, D.

Whll-length cDNA libraries and normalization
Unpublished

On Feb 15, 2001 this sequence version replaced gi:12894503.
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="let strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end entriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1077.f For
more information about this cluster, see
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5023.r For
nore information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODIO81CC06QPl&cluster=5023.r. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODIO81CC06QPl.
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cgi-bin/cluster.cgi?seq=CSODI012AG06QPl&cluster=1077.f. Contact
cgi-bin/cluster.cgi?seq=CSODI012AG06QPl&cluster=1077.f. Contact
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODI012AG06QPl.
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BP 191 91006 EVRY cedex - France
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/db_xref="taxon:9606"
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/mol type="maxN" of the property of the proper
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/db_xref="taxon:9606"
/clone="CSODF003YB02"
/tissue_type="FETAL BRAIN"
/dev_etage="fetal"
/dev_etage="fetal"
/clone lib="Homo sapiens FETAL BRAIN"
/note="Organ: brain; Vector: pCWVSPORT 6; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

a 295 c a 337 g 237 t 73 others
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BP 191 91006 EVRY cedex - France
Email: sequef@genoscope.cns.fr, Web
Library was constructed by Life Technologies, a division of
Invirogen. Contact : Feng Liang Email : fliang@lifetech.com URL:
http://fulllength.invirogen.com/ Invirogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBA007ZB09FF1.
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Li W. B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization
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Contact: Genoscope
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Pred. No. 6.5e+02;
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Genoscope - Centre National de Sequencage Genoscope.

BP 191 91006 ENRY cedex - France
BP 191 91006 ENRY cedex - France
BRail: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9817.f For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSDCC002AC03QPl&cluster=9817.f. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genisocope gequence ID: CSODC002AC03QPl.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Sases 1 to 1190)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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/mol_type="mRNA"
/db_xref="taxon:9606"
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//clone_TESODIO64VH04"
//clone_Tib="FLACENTA COT 25-NORMALIZED"
//clone_Tib="Homo sapiens PLACENTA COT 25-NORMALIZED"
//note="Ist strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCVVSPORT 6 vector. Library was normalized."

2.76 c 314 g 250 t 3.7 others
  pCMVSPORT 6 vector. Library was normalized."
226 g 257 t 58 others
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COT 25-NORMALIZED Homo sapiens CDNA
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1084)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
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BP 191 91006 EVRY cedex - France
Initial Every was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 5957.f For
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CS0DI064DD02QP1&cluster=5957.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI064DD02QP1.
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                                                                                                        Length 1060;
                                                                                                Score 20; DB 9; Length 106
Pred. No. 6.3e+02;
1; Mismatches 1; Indels
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/db_xref="taxon:9606"
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     sites of the 276 c
                                                                                                  80.0%;
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BX374761/c
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LOCUS
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/clone lib="Homo sapiens NEUROBLASTOWA"
/clone lib="Homo sapiens NEUROBLASTOWA"
/note="Vector: pcw/NSFORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
Library was nor normalized."
1 203 c 232 g 227 t 87 others
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/clone lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1060)
Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 3974.f For more information about this cluster, see http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CLOBB015ZG02FP1&cluster=3974.f. Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CLOBB015ZG02FP1.
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cgi-bin/cluster.cgi?seq=CSODI056BB11QP1&cluster=629.f. Contact
cgi-bin/cluster.cgi?seq=CSODI056BB11QP1&cluster=629.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI056BB11QP1.
Location/Qualifiers
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 629.f
more information about this cluster, see
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 9;
Pred. No. 6.2e+02
1; Mismatches
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                         /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CL0BB015ZG02"
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90.9%;
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Best Local Similarity
Matches 20; Congerv
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/clone=Tip="Homo sapiens PLACENTA COT 25-NORMA COT 25-NORM
                                                                                          EST 02-MAY-2003
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Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Introper. This sequence belongs to sequence cluster 334.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0D1005BE03QPI&cluster=334.r. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invir.orgen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI005BE03QPI.
                                                                       BX334648
BX334648 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
COT 25-NORMALIZED Homo sapiens CDNA
CLODE CSODIO05Y106 5-PRIME, mRNA sequence.
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1 (bases 1 to 933)
1 (bases 1 to 933)
1 (bases 1 to 934)
1 (bases 1 to 935)
1 (bases 1 to 938)
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Contact: Genoscope
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
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/clone_Tib="Homo sapiens NETROBLASTOMA COT 50-NORMALIZED"
/note="Ist strand cDNA was primed with a Not1-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCWNSPORT 6 vector. Library was normalized."

30c c 74 g 233 t 63 others
                                                                                                                                                                                                            /tissue_type="FETAL BRAIN"

/dev_stage="fetal"

/dov_stage="fetal"

/done_lib="Homo sapiens FETAL BRAIN"

/note="Organ: brain, vector: pCWWSPORT 6; 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."

1 211 carg was not normalized."
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910 bp mRNA linear EST 13-MAY-2003
BX395287 Homo sapiens NEUROBLASTOMA COT 50-NORMALIZED Homo sapiens
cDNA clone CS0DD004YF19 5-PRIME, mRNA sequence.
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1 (bases 1 to 910)
1 (Jul. W. Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Fong Liang Email : fliangblifetech.com URL
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODDO04CC10QP1.
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Genoscope - Centre National de Sequencage
1. 897
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                                                                                /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DF027YH18"
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Best Local Similarity 90.9
Matches 20; Conservative
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

RESULT 26

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FEATURES

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BASE COUNT ORIGIN

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Matches

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VERSION KEYWORDS SOURCE

AUTHORS TITLE

JOURNAL

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REFERENCE

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Contact: Genoscope
Contact: Genoscope
Genoscope - Centre National de Sequencage
Bp 191 91006 EVRY cedex. - France
Bp 191 91006 EVRY cedex. - France
Email: seqret@genoscope.ns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 9435.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-lan/cluster.cgi-StonDootAcG12QPl&cluster=9435.f. Contact :
Feng Liang Email: fliang@lifetech.com URL :
Feng Liang Email: fliang@lifetech.com URL :
Fraday Avenue Genoscope sequence ID : CSODD004CG12QPl.

Location/Qualifiers

Location/Qualifiers
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AL538354 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CS0DF027YHL8 5-FRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue type="NEUROBLASTOMA COT 50-NORMALIZED"
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/clone lib="Home sapiens NEUROBLASTOMA COT 50-NORMALIZED"
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primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCWVSPORT 6 vector. Library was normalized."
32 c library was normalized."
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 897)
Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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cgi-bin/cluster.cgi?seq=CSODF027DD09QPl&cluster=1734.r. Contact
cgi-bin/cluster.cgi?seq=CSODF027DD09QPl&cluster=1734.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenu Genoscope sequence ID : CSODF027DD03QPl.
Location/Qualifiers
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Contact: Genoscope
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                                                                                 1 (bases 1 to 894)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
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BP 191 91006 EVRY cedex - France
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
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/clone lihe="Homo sapiens B CELLS (RAMOS CELL LINE)"
/note="Vector: pcMvSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoNY sites of the pcMvSPORT 6 vector. Library was not normalized."
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                                                                                                                                                                                                                                                                                                                                              1006 bp mRNA linear EST 15-MAY-2003
CELLS (RAMOS CELL LINE) Homo sapiens cDNA
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
Li (bases 1 to 1006)
Li W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7333.f For
more information about this cluster, see
more information about this cluster, see
thtp://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOASOO9ZCO7QPl&cluster=7333.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://tullangth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOASOO9ZCO7QPl.
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                              Length 991;
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                           Score 20.2; DB 13;
Pred. No. 5.1e+02;
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BX428996 Homo sapiens B CELLS (RAMOS CELL : CLOOR GCODGO05YF18 5-PRIME, mRNA sequence.
BX428996
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
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                     80.8%;
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Homo sapiens (human)
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source

FEATURES

RESULT 24 BX333971/c

BASE COUNT

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VERSION KEYWORDS SOURCE

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Gaps

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Homo sapiens (human)
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/mol_type="mxnx,"
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/clone_Tb="mydector: pCWYSPORT 6; 1st strand cDNA was primed
/note="Vector: pCWYSPORT 6; vector: Library was not normalized." 7 others

28 c 234 g 220 t 7 others
                                                                                                                                                                                                                                                   Contact: Genoscope
Genoscope
Genoscope
Genoscope
BP 191 91006 EVRY cedex - France
Email: sequefocecope.cns.fr, Web : www.genoscope.cns.fr
Invitrogen. This sequence belongs to sequence cluster 6437.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSOCAP005DH01QP1&cluster=6437.r. Contact:
Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSOCAP005DH01QP1.
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                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. Li, Pages; I to 95, Jessee, J. and Polayes, D. Full-length, cDNA libraries and normalization
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7228.f For
more information about this cluster, see
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CSODM004YD15 5-PRIME, mRNA sequence.
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Local Similarity 88.0%; Pred. No. 5.1e+02;
les 22; Conservative 0; Mismatches 3;
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                      BX457051.1 GI:31034832
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BX457051
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BX422399/c
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Contact: Genoscope
Genoscope
Genoscope
Genoscope
BP 191 91006 EVRY cedex - France
Intoructed Policy of Sequence belongs to sequence cluster 6450.f

Invitrogen. This sequence luster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS2BAX17ZG05 AX28ZC12 l&cluster=6450.f.
Contact: Peng Liang Email: fliangelifetech.com URL:
contact: Peng Liang Email: fliangelifetech.com 1600
Faraday Avenue Genoscope sequence ID: CS2BAX17ZG05_AX28ZC12_1.
Location/Qualifiers
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205 c 218 g 260 t 3 others
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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25-NORMALIZED"
Feng Liang Email : fliang@lifetech.com URL :
http://fullIngth.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODMO04CB08QP1.
Location/Qualifiers
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BX345037.1 GI:30340331
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/lab.host="mind"
/lab.host="m
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602118471F1 NIH_MGC_56 Homo sapiens cDNA clone IMAGE:4275664 5',
mRNA sequence.
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                                                                                                                                                                                          /.clone_lb="MIH_MGC_95"
//clone_lb="NIH_MGC_95"
/note="Organ: brain; Vector: pBluescriptR (modified
pBluescript KS+); Site_l: BamHi; Site_2: Sall-KNoI (gtcgag
pBluescript KS+); Site_l: BamHi; Site_2: Sall-KNoI (gtcgag
j: oligo-dI primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
size-selected for average insert size_2: Skb and
normalized to ROT 5. This is a primary library enriched
for full-length clones and constructed using the
Cap-trapper method (Carninci, in preparation). Library
constructed by M. Brownstein (NIMH/NHGRI, National
Institutes of Health). Note: this is a NIH_MGC Library."
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Tissue Procurement: ATCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1094 row: n column: 17
High quality sequence stop: 589.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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Pred. No. 4.9e+02;
0; Mismatches 3; Indels 0:
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                                                                                                                                tissue_type="hippocampus"
/lab_host="DH10B"
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/mol_type="mRNA"
/db_xref="taxon:9606"
          organism="Homo sapiens"
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                                                                                                       /clone="IMAGE:5261647"
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                                      'mol_type="mRNA"
'db_xref="taxon:9606"
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/tissue type="NEUROBLASTONA"
/clone lib="Homo sapiens NEUROBLASTOMA"
/clone lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMWSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoxV sites of the pCMVSPORT 6 vector.
Library was not normalized." 6 others
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314 bp mRNA linear EST 12-WAY-2003
AL519260 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CSODA012YH14 5-PRIME, mRNA sequence.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 914)
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Genoscope - Centrar National de Sequencage
Benoscope - Centrar Parance
Brail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3874.r For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODA012DD07QP1&cluster=3874.r. Contact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CS0DA012DD07QP1. Location/Qualifiers
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clones and was constructed by Clontech s (Palo Alto, CA)." 247\ g 242\ t
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On Feb 13, 2001 this sequence version replaced gi:12782753
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                                                                                                                                                              Score 20.2; DB 10; Length 884;
Pred. No. 5e+02;
0; Mismatches 3; Indels 0
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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/organism="Homo sapiens"
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Ph.D.
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Location/Qualifiers
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Contact: Robert Strausberg, F
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Best Local Similarity
Matches 22; Conservat
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AUTHORS
TITLE
JOURNAL
COMMENT
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BI547007
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                 BG573114 10-APR-2001 02594115F1 NIH_MGC_79 Homo sapiens cDNA clone IMAGE:4721474 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol type="minny"
/db xref="taxon:8606"
/db xref="taxon:8606"
/db color="thage:472444"
/lab host="NHUB (T1 phage-resistant)"
/clone lib="NHH MGC 79"
/note="forgan: placenta; Vector: pDNR-LIB (Clontech);
Site 1: Sfil (ggccgcctcggcc); Site 2: Sfil (ggccattatggcc); 5, and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGCACAGT(ATO) byparate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.3 kb (range 0.5-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC library."
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 812)
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 706)
                                                                                                                                                                                                                                                                                                                                                Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nh.gov
Tissue Procurement: CLONTECH Laboratories, Inc.

cDNA Library Preparation: CLONTECH Laboratories, Inc.

clone Library Arrayed by: The I.M.A.G.E. Consortium(LINL)

found through the I.M.A.G.E. Consortium/LINL at:

cloud through the I.M.A.G.E. Consortium/LINL at:

Plate: LLCM1577 row: n column: 03

High quality sequence stop: 639.
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NATH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Homo sapiens
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Homo sapiens
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BF695849
                                                                     mRNA sequence.
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BF695849
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EST 05-SEP-2001
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Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tobnary Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMI1659 row: i column: 08
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 817)
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CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/Link at:
http://image.llnl.gov
Rlate: LicM929 row: m column: 01
High quality sequence stop: 637.
Location/Qualifiers
1. .812
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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1 Similarity 88.0%; Pred. No. 4.9e+02;
22; Conservative 0; Mismatches 3
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Full-length cDNA libraries and normalization
Unpublished
Contact: Ganoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Inbrary was conscructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 6911.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq-CSODC019BC08QP1&cluster=6911.r. Contact :
Feng Liang Email : fliang@llfetech.com URL :
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODC019BC08QP1.
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BP 191 91006 EVRY cedex - France
Inbarry was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7763.r For
http://www.genoscope.cns.fr/
http://www.genoscope.cns.fr/
Feng Liang Email: fliangaliferech.com URL:
http://fulllength.invitrogen.com/ InvitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODJOOIDCO60PI.
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CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
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1 (bases 1 to 1201)
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1 (Anno. Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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/clone="CS0DJ001YF12"
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/db_xref="taxon:9606"
/clone="CS0DC019YE16"
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11 (bases 1 to 645.noi.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                  /note="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the PCMVSPORT 6 vector. Library was normalized.

1 308 c 341 g 205 t
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603389227F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:5398255 5',
/cell line="JURKAT"
/clone lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
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Clone distribution: MGC clone distribution information can be clone through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
Plate: LLAM12015 row: e column: 08
High quality sequence stop: 643.
Location/Qualifiers
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Email: capbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
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/Lissue type="NEUROBLASTONA"
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/clone lib="Homo sapiens NEUROBLASTONA"
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with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
12 29 249 t
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BRail: sequenscope.one.fr, Web: www.genoscope.ons.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3923.f For
note information about this cluster, see
http://www.genoscope.ons.fr/
egi-bin/cluster.egi?seq=CLOBB018ZD09FP1&cluster=3923.f. Contact :
Feng Liang Email : fliang@alifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBB018ZD09FP1.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1145)
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/db_xref="taxon:9606"
/clone="CL0BB018ZD09"
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Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Brail: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

Invircogen. This sequence belongs to sequence cluster 6269.r For more information about this cluster, see

more information about this cluster, see

http://www.genoscope.cns.fr/

cgi-bin/cluster.cgi?seq=CS0DI062AD12QPl&cluster=6269.r. Contact:

Feng Liang Email: fliang@lifetech.com URL:

http://fulllength.invirrogen.com/ InvitroGen Corporation 1600

Faraday Avenue Genoscope sequence ID: CS0DI062AD12QPl.
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/dev stage="fetal"
/clone_lib="Home septemble FETAL BRAIN"
/note="Organ: brain; Vector: pCWVSBORT 6; 1st strand cDNA
was primed with a NotI-oligo (dT) primer. Five prime end
enriched, double-strand cDNA was digested with Not I and
cloned into the Not I and ECORV sites of the pCMVSBORT 6
vector. Library was not normalized."
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BX359829 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA
clone CSODI062YG23 5-PRIME, mRNA sequence.
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E 1 (Dasses 1 to 821)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished
Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Preparation: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
http://image.llnl.gov
Plate: LLCMAG.E. row: k column: 04
High quality sequence stop: 816.

Location/Qualifiers

Location/Qualifiers
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/lab host="DHIOB (phage-resistant)"
/lone_line="NHHOG do phage-resistant)"
/note="Organ: prostate; Vector: porB7; Site_1: XhoI;
/note="Organ: prostate; Vector: porB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following s' adaptor: GGCACGAG (G). Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MCC Library."
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602649914T1 NIH_MGC_40 Homo sapiens CDNA clone IMAGE:4760955 3',
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/db_xref="taxon:9606"
/clone="IMAGE:4760955"
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834 bp mRNA linear EST 15-MAY-2003
BX441089 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
CSODF014YA08 5-PRIME, mRNA sequence.
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/dev_stage="fetal"
/clone_lib="Momo sales FETAL BRAIN"
/note="Organ: brain; Vector: pCWVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECORV sites of the pCMVSPORT 6 vector. Library was not normalized."

214 c 222 g 240 t 11 others
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library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2850.r For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODF014BA04Qpl&cluster=2850.r. Contact :
Feng Liang Email: fliangelifetech.com URL:
http://fulllength.invitrogen.com/ InvitroGen. Corporation 1600
Faraday Avenue Genoscope sequence ID: CSODF014BA04QPl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODF038DF09QP1&cluster=2189.r. Contact :
Feng Liang Email : fliangalifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODF038DF09QP1.
Location/Qualifiers
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 917)
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 2189.r For
more information about this cluster, see
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                                                                                  1 (bases 1 to 917)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replaced gi:12800068.
Contact: Genoscope
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:960g"
/clone="CSODF038YL18"
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Gaps

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/mol_type="mRNA"
/strain="No.
/db_xref="taxon:6239"
/db_xref="taxon:6239"
/sca="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/note="The AD-wrmcDNA"
/n
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Contact: Genoscope
Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
5973.r For more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODH006BC00QP1&cluster=5973.r. Contact :
Feng Liang Email: fliangalifetech.com URL:
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODH006BC08QP1.
Location/Qualifiers

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AL557510 Homo sapiens T CELLS (JURKAT CELL LINE) Homo sapiens CDNA clone CSODH006YE16 5-PRIME, mRNA sequence.

AL557510.2 GI:31279310
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1. (bases 1 to 801)

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished
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Best Local Similarity 95.5
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Genorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.

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Davy, A., Bello, P., Thierry-Mieg, N., Vaglio, P., Hitti, J.,
Doucette-Stamm, L., Thierry-Mieg, D., Reboul, J., Boulton, S., Walhout
, A.J., Coux, O. and Vida, Mann of the Caenorhabditis elegans 26S
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/ tissue_type="whole animal"
/ dev stage="mixed stage"
/ clone_lib="AD-wrmcDNA"
/ note="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"
a 139 c 146 g 144 t
         protein-protein interaction map of the Caenorhabditis elegans 26S
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Tel: 617 632 5180
Fax: 617 632 5739
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Dana Farber Cancer Institute
Limmy Fund Way Smith 858, BOSTON, MA 02115,
Tel: 617 632 5180
Fax: 617 632 5739
Fax: 617 632 5739
Fax: 617 632 5739
Figure dyployst.x with Bait unknown
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/mol_type="mRNA"
/strain="N2"
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Marc Vidal Laboratory
Dana Farber Cancer Institute
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 4354.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=GSOBAK021BF12NM1&cluster=4354.f. Contact:
Feng Liang Email: filiang@lifetech.com/URL
Faraday Avenue Genoscope sequence ID: CSOBAK021BF12NM1.
Location/Qualifiers
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                                                                                                                                   /tissue_type="NEUROBLASTOMA_COT_SO-NORMALIZED"
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/note="Ist strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."
a 291 c 107 g 373 t 13 others
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BX329816 Homo sapiens NEUROBLASTOWA COT 50-NORMALIZED Homo sapiens CDNA COT 50-NORMALIZED Homo sapiens CDNA clone CSODD005YC15 3-PRIME, mRNA sequence.
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Li (bases 1 to 996)
Li W. B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
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                                                                                                                                                                                                                                                                                                           Score 21.2; DB 13; Length 1201; Pred. No. 2e+02; 1; Mismatches 0; Indels 0;
     Faraday Avenue Genoscope sequence ID : CSODD006BC04QP1.
Location/Qualifiers
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Pred. No. 2.9e+02;
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                                                                               /mol_type="mRNA"
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91.7%;
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95.5%;
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Best Local Similarity
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AUTHORS
TITLE
JOURNAL
COMMENT
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BX329816
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KEYWORDS
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Gaps

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Indels

0; Mismatches

Conservative

22; N

Matches

25

TTCAGCTTTCTTGTACAAACTTGT

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/tissue type="NEUROBLASTOWA"
//cione lib="Homo sapiens NEUROBLASTOWA"
/note="Vector: PCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and ECRY sites of the pCMVSPORT 6 vector. Library was not normalized."
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EST. 28-JAN-2003
CB104071.1 GI:27929878
EST.
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1 (bases 1 to 598)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Bmail: seqrefégenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 1606.r For
nore information about this cluster, see
http://www.genoscope.cns.fr/
egi-bin/cluster.cgi?seq=CLOBB019ZB04FP1&cluster=1606.r. Contact :
Feng Liang Email : fliangalifetech.com URL :
http://tulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBB019ZB04FF1.
                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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AL515389 Homo sapiens NEUROBLASTOMA Homo sapiens CDNA Clone CLOBB0192804 3-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                         1 (bases 1 to 559)
Li.M.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
On Feb 13, 2001 this sequence version replace
Contact: Genoscope
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November 6, 2003, 22:08:13; Search time 1093.75 Seconds (without alignments) 555.531 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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21.2 20.8 20.4 20.4

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CB104084 ADP SQ015 AL557510 AL557510 BG775435 G02549914 AL536575 AL536575 BX441089 BX441089 BX359829 BX559829 AL515949 AL515449 BX394655 BX394655 BX361644 BX361644 B1858895 G03389227 BG573114 G02594115 BF695849 G01190229	AL519260 AL512470  AL519260 AL512960  BX457051 BX472399  BX428396 BX428996  BX333971 BX333971  AL538354 AL538354  BX335287 BX335287  BX334648 BX335287  AL514767 AL514767  AL550767 AL550767  BX33865 BX33865  BX33865 BX33865  BX33865 BX33865  BX45147 BX34641  AL51477 AL513677  AL51477 BX33865  BX463747 BX463747  AL51477 BX554071  BX463747 BX38656  BX363509 BX365509  BX363509 BX365509  BX363509 BX365509  BX3633409 952062A07  BQ4163507 952079D01  BQ163507 952079D01	LIGNMENTS  201 bp mRNA linear EST 08-MAY-2003  ROBLASTOMA COT 50-NORMALIZED Homo sapiens -PRIME, mRNA sequence.  e.J. and Polayes, D. s and normalization  al de Sequencage France ns.fr, Web: www.genoscope.cns.fr y Life Technologies, a division of belongs to sequence cluster 2992.f For is cluster, see fr ff/ ff/ SODDOOSBC04QP1&cluster=2992.f. Contact: Glifetech.com URL: Glifetech.com URL: Glifetech.com URL: Gen.com/ InvitroGen Corporation 1600
CB104084 AL557510 BG775435 AL536575 BX441089 BX359829 BX35849 BX364655 BX361644 BR6658895 BX361644 BR6658895	ALF66996 BX452299 BX422399 BX422399 BX4283961 BX533371 BX53334648 BX3334648 BX334648 BX334648 BX34648 BX546377 AL514761 BX546371 AL514071 AL54923 AL54923 AL54923 AL54071 BX540993 BX386369 BX386369 BX386369 BX386369 BX386369 BX386369 BX386369 BX386369 BX463202 BX463202 BX463202 BX463202 BX463202 BX463202 BX463202 BX463202 BX463202	A 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
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RESULT 40
US-09-907-900-42
; Sequence 42, Application US/09907900
; Patent No. US202020172997A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; APPLICANT: Temple, Gary F.
; APPLICANT: Temple, Gary F.
; APPLICANT: Temple, Gary F.
; TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having
; TITLE OF INVENTION: Recombination Sites
; TITLE OF INVENTION: Recombination Sites
; FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,900
; CURRENT PILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIN Ver. 2.0
; SEQ ID NO 42
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE: OTHER INFORMATION: Description of Unknown Organism: recombination OTHER INFORMATION: products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
90.4%; Score 22.6; DB 10;
Best Local Similarity 76.0%; Pred. No. 3.1;
Matches 19; Conservative 6; Mismatches 0;
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ORGANISM: Unknown
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US-09-855-797A-42

i Sequence 42, Application US/09855797A
; Sequence 42, Application US/09855797A
; GENERAL INFORMATION:
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombination Sites
FILE REFERRINCE: 0942.2850008
FURRENT APPLICATION NUMBER: 08/09/855,797A
CURRENT FILING DATE: 1999-04-22
PRIOR APPLICATION NUMBER: 09/296,281
PRIOR PLING DATE: 1999-10-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42
LINGHH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9; Length 43;
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93.6%; Score 23.4; Di
Best Local Similarity 96.0%; Pred. No. 1.6;
Matches 24; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 Gricagciricrigiacaacrigi 5
                                                                                    Sequence 45, Application US/09732914
Patent No. US20020007051A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: attR2 PCR Primer US-09-732-914-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: Unknown
                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Cheo, L
                                                        US-09-732-914-45/c
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Gaps

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Length 25; Indels

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 23.4; DB 14;
Pred. No. 1.4;
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PUDLICATION NO. US20030119104A1

PUDLICANT: PETKINS, Edward

APPLICANT: Perez, Carl

APPLICANT: Lindenbaum, Michael

APPLICANT: Lindenbaum, Michael

APPLICANT: Leung, Josephine

APPLICANT: Fleming, Elena

APPLICANT: Stewart, Sandra

APPLICANT: Shellard, Joan

TILLE APPLICANT: Stellard, Joan

TILLE REFERENCE: 24601-420

CURRENT APPLICATION NUMBER: US/10/161,403

CURRENT FILING DATE: 2002-05-30

PRIOR APPLICATION NUMBER: 60/294,758

PRIOR APPLICATION NUMBER: 60/366,891

PRIOR FILING DATE: 2001-05-30

PRIOR FILING DATE: 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Mismatches
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/432,085
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                           FILING DATE: *UNKNOWN>
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/05,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
FILING DATE: 07-JUN-1995
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: DOLD

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-162-879-10
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                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        93.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: both
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Best Local Similarity 96.0
Matches 24; Conservative
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ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington STATE: DC
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C STREET: 1100 New York Ave., N. W. Suite 600 CITY: Washington STATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 14; Length 25;
                                                                                                                COUNTRY: USA
COUNTRY: USA
COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FO Compatible
OPENATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/162,879
FILING DATE: 06-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 23.4; DB Pred. No. 1.4; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/432,085
FILING DATE: 1999-11-02
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 09/005,476
FILING DATE: 07-JAN-1998
APPLICATION NUMBER: 08/63,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: both

MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-058-292-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GITCAGCTITITIGIACAAACTIGI 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 202-371-2540
N FOR SEQ ID NO: 10:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 93.6%;
Best Local Similarity 96.0%;
Matches 24; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: both
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RESULT 35
US-10-058-292-10
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US-10-055-001A-5
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                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                            Matches
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                                            08/486,139
FILING DATE: 07-JUN-1996

CLASSIFICATION D.

RICHASTICATION DATA:
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
CLASSIFICATION:
TELECOMMUNICATION: 1NFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: 10:
SEQUENCE CHARACTERICICS:
LENGTH: 25 base pairs
TYPE: MUCLEIC acid
TYPE: MUCLEIC acid
TYPE: MUCLEIC acid
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96.0%;
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                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 96.0%;
Matches 24; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 96.0°
                                                                                                                                                                                                               MOLECULE TYPE: CDNA
                                                                                                                                                                                                  TOPOLOGY: both
                                                                                                                                                                                                                                                                                                                 1 GTTCAGCT
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ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 33
US-10-300-892-10
                                                                                                                                                                                                                                                                                                                                                                                                    US-09-985-448-10
                                                                                                                                                                                                                              US-09-432-085-10
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Sequence 5, Application US/10055001A

Sequence 5, Application US/10055001A

Publication No. US20030049835A1

SEGUENBAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Helliwell, Christopher A.
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE OF INVENTION: using recombinational cloning
FILE REPREFANCE: HELGA

CURRENT PILLING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 5
LENTH: 25
LENTH: 25
LENTH: 25
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APPLICANT: Fox, Donna K.

TITLE OF INVENTION: Recombinational Cloning Using Nucleic Acids Having TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/10/300,892
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/907,719
PRIOR APPLICATION NUMBER: US/09/907,719
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/10058292
Publication No. US20030054552A1
GENERAL INFORMATION:
APPLICANT: Hartley, James L.
Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of Unknown Organism: recombination; OTHER INFORMATION: products
US-10-300-892-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 25;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 23.4; DB 12;
Pred. No. 1.4;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 93.6%;
1. Similarity 96.0%;
24; Conservative
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best_Local Similarity
Matches 24; Conserv
                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Unknown
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FILING DATE: 13 CLASSIFICATION:
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                                                      JS-09-907-719-10
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STATE:
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| Sequence 10, Application US/09907900
| Patent No. US20020172937A1
| GENERAL INFORMATION:
| APPLICANT: Hartley, James L. |
| APPLICANT: Hartley, James L. |
| APPLICANT: Temple, Gary F. |
| TITLE OF INVENTION: Recombination Sites |
| TITLE OF INVENTION NUMBER: US/09/907,900 |
| CURRENT APPLICATION NUMBER: 09/177,387 |
| PRIOR FILING DATE: 1998-10-23 |
| NUMBER OF SEQ.ID NOS: 60 |
| SEQ.ID NO 10 |
| LEMETH: 25 |
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                              Sequence 10, Application US/09855797A
; Sequence 10, Application US/09855797A
; Patent No. US20020094574A1
; GENERAL INFORMATION:
    APPLICANT: Hartley, James L.
    APPLICANT: Brasch, Michael A.
    APPLICANT: Temple, Gary F.
    APPLICANT: 200108
; CURRENT APPLICATION NUMBER: 09/296,281
FRIOR FILING DATE: 1999-10-24
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTHER INFORMATION: Description of Unknown Organism: recombination of Unknown Organism: recombination products US-09-855-797A-10
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Local Similarity 96.0%; Pred. No. 1.4;
les 24; Conservative 0; Mismatches
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Best Local Similarity 96.vv
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ORGANISM: Unknown
FEATURE:
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ORGANISM: Unknown
FEATURE:
RESULT 28
US-09-855-797A-10
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Matches
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Sequence 10, Application US/09907119
; Sequence 10, Application US/09907119
; Publication No. US20020192819A1
; GENERAL INFORMATION:
    APPLICANT: Hartley, James L.
    APPLICANT: Temple, Gary F.
    APPLICANT: Pox, Donna K.
    TITLE OF INVENTION: Recombination Sites
    FILE REFERENCE: 0942.2850004
; CURRENT APPLICATION NUMBER: US/09/907,719
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US/09/177,387
; RIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: Patentin Ver. 2.0
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US-09-907-719-10
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APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Harsh, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
TITLE OF INVENTION: Recombination Sites
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C
STREET: 1100 New York Ave., N. W. Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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PAPLICATION NUMBER: US/09/432,085 FILING DATE: (Herewith)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 93.6%; Score 23.4; DB 10; Best Local Similarity 96.0%; Pred. No. 1.4; Matches 24; Conservative 0; Mismatches 1;
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ZIP: 2005-3934
COMPUTER READABLE FORM:
MEDUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
CLASSIFICATION:
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12-JAN-1998
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APPLICATION NUMBER:
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RESULT 26

105-10-055-001A-26

1 Sequence 26, Application US/10055001A

2 Sequence 26, Application US/10055001A

2 Beducation No. US20030049835A1

3 GENERAL INNORMATION:

APPLICANT: Wasley, Susan V.

APPLICANT: Waterhouse, Peter

APPLICANT: Helliwell, Christopher A.

TITLE OF INVENTION: Washer accombinational cloning

TITLE OF INVENTION: Using recombinational cloning

FILE REFERENCE: HELGA

CURRENT FILING DATE: 2002-06-11

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin version 3.1

SEQ ID NO 26

LENGTH: 17681
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US-10-055-001A-26/c
US-10-055-001A
Squence 26, Application US/10055001A
Publication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE OF INVENTION: Using recombinational cloning
FILE REFERENCE: HELLGA
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Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
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     Length 17476;
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Query Match
100.0%; Score 25; DB 14;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0;
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US-10-055-001A-26
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US-10-055-001A-26
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CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
SEQ ID NO 26
LENGTH: 17681
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Matches 25; Conserv
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US-10-055-001A-24/c
Squence 24, Application US/10055001A
Fublication No. US20030049835A1
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wesley, Susan V.
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: Method and means for producing efficient silencing constructs;
TITLE OF INVENTION: Wesley, TITLE OF STREET HELICA.
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOCTIONS OF THE NOS: 26
SOCTIONS OF THE NEST OF THE NOS: 26
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Sequence 24, Application US/10055001A

Publication No. US2030049835A1

Publication No. US2030049835A1

Publication No. Wesley, Susan V.

APPLICANT: Wesley, Susan V.

APPLICANT: Wesley, Susan V.

TITLE OF INVENTION: Method and means for producing efficient silencing constructs

TITLE OF INVENTION: Wind recombinational cloning

FILE REFERENCE: HELLGA

CURRENT APPLICATION NUMBER: US/10/055,001A

CURRENT PILING DAIR: 2002-06-11

NUMBER OF SEQ ID NOS: 26

SOFUTION 24

LENGTH: 17476
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Best Local Similarity 100.0%; Pred. No. 0.95;
Bact Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                             Length 17476;
                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                          Query Match
100.0%; Score 25; DB 12;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ) OTHER INFORMATION: acceptor vector pHELLSGATE8
US-10-055-001A-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: acceptor vector phallsGales
                                                                                                                                                                                                                                                                                                                                                                 13050 GTTCAGCTTTTTGTACAACTTGT 13026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16674 Gricagcriririgiacaaacrigi 16698
                                                                                                                                    FEATURE:
, OTHER INFORMATION: plasmid pHELLSGATE 8
US-10-385-546-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GITCAGCTITITIGIACAAACTIGT 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Artificial sequence
          SOFTWARE: Patentin version 3.0 SEQ ID NO 7 LENGTH: 17476
                                                                                      TYPE: DNA ORGANISM: Artificial
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LENGTH: 17476
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APPLICANT: Wesley, Susan
APPLICANT: Wesley, Susan
APPLICANT: Wesley, Susan
APPLICANT: Helliwell, Chris
TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
FILE REFERENCE: COLINA-US2
CURRENT APPLICATION NUMBER: US/10/385,546
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION UNDER: US 60363852
PRIOR APPLICATION UNDER: US 60363852
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Waterhouse, Peter
APPLICANT: Wesley, Susan
APPLICANT: Helliwell, Chris
TITLE OF INVENTION: Methods and means for monitoring and modulating gene silencing
FILE REFERENCE: COLINA-US2
APPLICANT: Helliwell, Christopher A.

TITLE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE OF INVENTION: using recombinational cloning
FILE REFERENCE: HELLGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
100.0%; Score 25; DB 14; Length 17458;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: acceptor vector pHELLSGATE11
US-10-055-001A-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13050 GTTCAGCTTTTTTGTACAACTTGT 13026
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/385,546
CURRENT FILING DATE: 2003-03-12
PRIOR APPLICATION NUMBER: US 60363852
PRIOR FILING DATE: 2003-03-14
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: plasmid pHELLSGATE 8 US-10-385-546-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/10385546 Publication No. US20030175783A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                              ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial
                                                                                                                                                                                                                  SEQ ID NO 25
LENGTH: 17458
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LENGTH: 17476
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US-10-385-546-7/c
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                                                                                                                                                                                                                                                                          TYPE: DNA
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US-10-055-001A-25
s Gaquence 25, Application US/10055001A
publication No. US20030049835A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Method and means for producing efficient silencing constructs
TITLE OF INVENTION: Wethod and means for producing efficient silencing constructs
TITLE OF INVENTION: Wethod and means for producing efficient silencing constructs
TITLE OF INVENTION: Using recombinational cloning
FILE REFERENCE: HELIGA
CURRENT PRILIG DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEQ ID NO 25
INNUMBER 17458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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                                                                        APPLICANT: Zhu.T.
APPLICANT: Zhu.T.
APPLICANT: Han, B.
APPLICANT: Han, B.
APPLICANT: Han, B.
APPLICANT: Cooper. Bret
TITLE OF INVENITON: Promoters for regulation of plant expression
FILE REFERENCE: 1360.001UG1
CURRENT APPLICATION NUMBER: US/09/887,576
CURRENT FILING DATE: 2000-06-25
PRIOR APPLICATION NUMBER: US 60/213,848
PRIOR APPLICATION NUMBER: US 60/214,087
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-06-23
PRIOR PILING DATE: 2000-16-29
PRIOR PILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 875
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 811
LENGTH: NANA
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100.0%; Score 25; DB 14; Length 17458;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 10; Length 11180; 100.0%; Pred. No. 0.88; 0; Indels 0;
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OTHER INFORMATION: acceptor vector pHELLSGATE11
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Publication No. US20030049835A1
GENERAL INFORMATION:
APPLICANT: Wealey, Susan V.
APPLICANT: Waterhouse, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Artificial sequence
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     Budworth, P.
Brown, D.
Chang, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 25; Conserv
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US-10-055-001A-25/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: gene
LOCATION: (1426)..(1510)
OTHER INFORMATION: inactivated ccdA
                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: plasmid pDEST1
                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: gene
LOCATION: (216)...(257)
OTHER INFORMATION: Trc promoter
                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Artificial sequence
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Best Local Similarity 100.0
Matches 25; Conservative
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LOCATION: (5340)..(6420)
OTHER INFORMATION: lacIq
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NAME/KEY: gene
LOCATION: (4104) .. (4264)
OTHER INFORMATION: ori
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LOCATION: (273)..(393)
OTHER INFORMATION: attR1
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OTHER INFORMATION: attR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: gene
LOCATION: (2598)..(3503)
OTHER INFORMATION: ampR
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LOCATION: (4504)..(4941)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1648) . (1953)
OTHER INFORMATION: ccdB
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LOCATION: (647)..(1306)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OTHER INFORMATION: CMR
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US-09-887-576-581/c
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NAME/KEY: gene
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                                                                                                                                                                                                                                                                                                                                 Length 1846;
                                                                                                                                                                                                                                                                                                                                 Query Match
100.0%; Score 25; DB 14; Length 1
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 25; Conservative 0; Mismatches 0; Indels
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US-10-241-590-13//C

Publication No. UG20030166238A1

GENERAL INPORMATION:

APPLICANT: Microbiological Research Authority

APPLICANT: The Speywood Laboratory Limited

TITLE OF INVENTION: Recombinant Toxin Fragments

FILE REFERENCE: 1581.013003

CURRENT APPLICATION NUMBER: US/10/241,596

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 09/255,829

PRIOR APPLICATION NUMBER: US 09/255,829

PRIOR APPLICATION NUMBER: US 09/255,829

PRIOR FILING DATE: 1999-02-3

PRIOR FILING DATE: 1999-02-3

PRIOR FILING DATE: 1997-08-23

PRIOR FILING DATE: 1997-08-23

PRIOR FILING DATE: 1996-12-77

PRIOR PRILING DATE: 1996-12-77

PRIOR FILING DATE: 1996-12-77

PRIOR FILING DATE: 1996-12-77

PRIOR FILING DATE: 1996-08-23

NUMBER OF SEQ ID NOS: 175

SEQ ID NO 137

LENGTH: S558
FILE REFERENCE: A-70174-1/RFT/RMS/RWK
CURRENT APPLICATION NUMBER: US/10/023,208
CURRENT FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: US 60/256,163
PRIOR FILING DATE: 2000-12-14
NUMBER OF SEQ ID NOS: 63
SOFTWARE: Patentin version 3.1
SOFTWARE: Patentin version 3.1
LENGTH: 1846
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Publication No. US20030124555A1;
GENERAL INFORMATION:
APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
APPLICANT: LI, XIAO
APPLICANT: ESPOSITO, DOMINIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Clostridium botulinum
US-10-241-596-137
                                                                                                                                                                                                        TYPE: DNA ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                              ; OTHER INFORMATION: synthetic US-10-023-208-63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 25; Conserv
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US-10-151-690-20/c
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APPLICANT: LI, XIAO
APPLICANT: ESPOSITO, DOMINIC
APPLICANT: ESPOSITO, DOMINIC
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOD
FILE REFERENCE: 0942.5120001
FULE REFERENCE: 0942.5120001
FULE REPERENCE: 0942.5120001
FULE REPERENCE: 0942.5120001
FULE REPERENCE: 0942.5120001
FRIOR PELICATION NUMBER: US 10/151,690
FRIOR FILING DATE: 2002-05-21
FRIOR FILING DATE: 2002-05-21
FRIOR FILING DATE: 2002-05-21
APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in TITLE OF INVENTION: Use of Multiple Recombination Sites with Unique Specificity in TITLE OF INVENTION: Recombinational Cloning
FILE REFERENCE: 0942.5010002
CURRENT APPLICATION NUMBER: US 60/99/32,914
CURRENT APPLICATION NUMBER: US 60/169,983
PRIOR PELING DATE: 1999-12-10
PRIOR PELING DATE: 1999-12-10
PRIOR PILING DATE: US 60/188,020
PRIOR PAPLICATION NUMBER: US 60/188,020
NUMBER OF SEQ ID NOS: 140
SEQ ID NO 94
SEQ ID NO 44
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
100.0%; Score 25; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 25; Conservative 0; Mismatches 0; Indels
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Publication No. US20030124537A1
GENERAL INFORMATION:
APPLICANT: Li, Min
APPLICANT: Liu, Yuan-Ching
TITLE OF INVENTION: PROCARYOTIC LIBRARIES AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GITCAGCITITIGIACAACTIGI 25
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Publication No. US2003012455A1
GENERAL INFORMATION:
APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; OTHER INFORMATION: plasmid pDEST1
US-10-151-690-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 64
SOFWRARE: Patentin version 3.1
SEQ ID NO 19
LENGTH: 120
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                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA ORGANISM: attR1 PCR Primer
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Best Local Similarity
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US-10-151-690-19/c
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US-10-023-208-63/c
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                                                                         APPLICANT: BRASCH, MICHAEL A.
APPLICANT: BRASCH, MICHAEL A.
APPLICANT: CHEO, DAVID
APPLICANT: CHEO, DAVID
APPLICANT: CHEO, DAVID
APPLICANT: BSPOSITO, DOMINIC
APPLICANT: BYED, DEVON R.N.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOL
FILE REPERENCE: 0942.5120001
CURRENT FILING DATE: 2002-05-21
CURRENT FILING DATE: 2002-05-21
FRIOR FILING DATE: 2002-05-21
FRIOR FILING DATE: 2001-05-21
FRIOR FILING DATE: 2001-05-21
NUMBER OF SEQ ID NOS: 64
SSEQ ID NO 32
ILENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 25; DB 14; Length 25; Pred. No. 0.3;
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; Sequence 33, Application US/09974760B
; Publication No. US2003014370SA1
; GENERAL INFORMATION:
; APPLICANT: Sherman, Amir
; APPLICANT: Trucherart, Joshua
; APPLICANT: Trucherart, Joshua
; APPLICANT: Trucherart, Joshua
; APPLICANT: Halle, G. Todd
; TITLE OF INVENTION: LOVE VARIANT REGULATOR MOLECULES
; FILE REPERENCE: 14184-009001
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PastSEQ for Windows Version 4.0
; SEQ ID NO 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 25; DB Best Local Similarity 100.0%; Pred. No. 0.3 Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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Patent No. US20020007051A1
GENERAL INFORMATION:
APPLICANT: Cheo, David
APPLICANT: Brasch, Michael A.
APPLICANT: Temple, Gary F.
          Sequence 32, Application US/10151690 Publication No. US20030124555A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 100.
Matches 25; Conservative
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                                    Publication No. US200
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA; ORGANISM: attR1 US-10-151-690-32
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US-09-732-914-44/c
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Derez, Carl
APPLICANT: Lindenbaum, Michael
APPLICANT: Lindenbaum, Michael
APPLICANT: Leung, Josephine
APPLICANT: Fleming, Blena
APPLICANT: Stewart, Sandra
APPLICANT: Shellard, Joan
TILLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
FILL OF PRINCE 24601-420
CURRENT APPLICATION NUMBER: US/10/161,403
CURRENT APPLICATION NUMBER: 00/294,758
PRIOR FILLING DATE: 2001-05-30
PRIOR FILLING DATE: 2001-05-30
PRIOR FILLING DATE: 2002-03-31
NUMBER OF SEQ ID NOS: 129
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
FILING DATE: <UNKNOWN>
APPLICATION NUMBER: 09/233,493
FILING DATE: 20-JAN-1999
APPLICATION NUMBER: 09/005,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 08/63,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELERGONMUNICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELERGONMUNICATION NUMBER: 08/486,139
FILING DATE: 07-JUN-1995
TELERGONMUNICATION: TELERGONG: 202-371-2600
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                             1 GITCAGCITITITGIACAAACTIGI 25
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Best Local Similarity 100.0%; P. Matches 25; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 100.0
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Perkins, Edward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: attR1 US-10-161-403-49
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US-10-161-403-49
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; Publication No. US20030068799A1
; GENERAL INFORMATION:
; APPLICANT: Hartley, James L.
; TITLE OF INVENTION: Recombinational Cloning Using Engineered
; Recombination Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 100.0%; Score 25; DB 14; Length 25; Best Local Similarity 100.0%; Pred. No. 0.3; Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/058,292
FILING DATE: 30-Jan-2002
CIASSIFICATION NUMBER: 09/432,085
FILING DATE: 1999-11-02
APPLICATION NUMBER: 09/233,493
FILING DATE: 1999-1998
APPLICATION NUMBER: 09/05,476
FILING DATE: 12-JAN-1998
APPLICATION NUMBER: 09/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 08/663,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 09/396,002
FILING DATE: 07-JUN-1996
APPLICATION NUMBER: 09/396,002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 2005-394
COMPUTER EADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX,
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
STRATE: DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/162,879
FILING DATE: 06-Jun-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/432,085
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MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-058-292-9
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                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 202-371-2540 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 25 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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       STATE: DC
COUNTRY: USA
ZIP: 20005-3934
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US-10-162-879-9
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Best Local Similarity
Matches 25; Conserv
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COTHER INFORMATION:
US-10-300-892-9
                                                                                                                              TYPE: DNA
ORGANISM: Unknown
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US-10-058-292-9
                                                                                                      SEQ ID NO 9
LENGTH: 25
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100.0%; Score 25; DB 12; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                           DB 11;
                                                                                                                                                                           100.0%; Score 25; DE ilarity 100.0%; Pred. No. 0.3 Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GTTCAGCTTTTTTGTACAAACTTGT 25
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                                                                                                                                                                                                                                          1 GTTCAGCTTTTTTGTACAAACTTGT 25
  08/486,139
                                TELECOMMUNICATION INFORMATION:
TELEPAK: 202-371-260
TELEPAK: 202-371-2540
TELEPAK: 202-371-2540
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECTLE TYPE: CDNA
US-09-432-085-9
            07-JUN-1995
APPLICATION NUMBER:
FILING DATE: 07-JUN
CLASSIFICATION:
                                                                                                                                                                         Query Match
Best Local Similarity
Matches 25; Cönserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-10-300-892-9
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Sequence 4, Application US/10055001A

Sequence 4, Application US/10055001A

Publication No. US20030049835A1

GENERAL INFORMATION:
APPLICANT: Waterhouse, Peter
APPLICANT: Waterhouse, Peter
APPLICANT: Helliwell, Christopher A.
TITLE OF INVENTION: using recombinational cloning
FILE REPERENCE: HELGA
CURRENT APPLICATION NUMBER: US/10/055,001A
CURRENT FILING DATE: 2002-06-11

SEQ ID NO 4

LEMOTH: 25

LEMOTH: 25
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Brasch, Michael A.
TITLE OF INVENTION: Recombinational Cloning Using Engineered
Recombination Sites
                                                                                                                                                                                                                                                                                                                                     Description of Unknown Organism: recombination products
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Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: core sequence of recombination site attR1 US-10-055-001A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 25;
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CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX,
STREET: 1100 New York Ave., N. W. Suite 600
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 100.0%; Score 25; DB 12; Similarity 100.0%; Pred. No. 0.3; 25; Conservative 0; Mismatches 0;
FILE REFERENCE: 0942.2850004
CURRENT APPLICATION NUMBER: US/10/300,892
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US/09/907,719
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR APPLICATION NUMBER: US/09/177,387
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PATENTIN VEY: 2.0
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; Publication No. US20030054552A1
; GENERAL INFORMATION:
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ORGANISM: Artificial sequence
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; Sequence 9, Application US/09907900
; Ratent No. US2002012297A1
; GENERAL INFORMATION:
   APPLICANT: Hartley, James L.
   APPLICANT: Hartley, Gary F.
   APPLICANT: Temple, Gary F.
   APPLICANT: Temple, Gary F.
   APPLICANT: Temple, Gary F.
   APPLICANT: Dona K.
   TITLE OF INVENTION: Recombination Sites
   TITLE OF INVENTION: Recombination Sites
   TITLE OF INVENTION Recombination Sites
   TILE REFERENCE: 0942_2850004
   CURRENT APPLICATION NUMBER: US/09/907,900
   CURRENT APPLICATION NUMBER: 09/177,387
   PRIOR APPLICATION NUMBER: 09/177,387
   NUMBER OF SEQ ID NOS: 60
   SOFTWARE: PatentIN Ver. 2.0
   SOFTWARE: PatentIN Ver. 2.0
   SEQ ID NO 9
                 APPLICANT: Hartley, James L.
APPLICANT: Hartley, James L.
APPLICANT: Brackl, Michael A.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
APPLICANT: Temple, Gary F.
TITLE OF INVENTION: Recombination Sites
TITLE OF INVENTION: Recombination Sites
FILE REFERENCE: 0942.2850008
CURRENT APPLICATION NUMBER: US/09/855,797A
CURRENT FILING DATE: 2001-05-16
PRIOR PRICATION NUMBER: 09/296,281
PRIOR PLILOR DATE: 1999-04-22
PRIOR PLILOR DATE: 1999-04-24
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.0
SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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US-09-907-900-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) OTHER INFORMATION: Description of Unknown Organism: recombination; OTHER INFORMATION: products
US-09-855-797A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 25; DB 9; Length 25; 100.0%; Pred. No. 0.3; cive 0; Mismatches 0; Indels
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Best Local Similarity 100.0
Matches 25; Conservative
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US20020094574A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA ORGANISM: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
US-09-907-900-9
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RESULT 4 US-09-907-719-9

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Pacipaces 9, Application US (09997179)
Publication No. U2200018219A1
APPLICANT: Hartley, Admes L.
APPLICANT: Hartley, Admes L.
APPLICANT: Hartley, Admes L.
APPLICANT: Hartley, Admes L.
APPLICANT: Pemple, Admy Recombination Cloning Using Nucleic Acids Having TTTLE DE TWENTION: Recombination Sites
TTTLE PREFERENCE: 0942.290014719
FULD REPLICANTON NUMBER: US/09/20717,387
FULD REPLICANTON NUMBER: US/09/2005
FRESULT S
FULD REPLICANTON NUMBER: US/09/2005
FULD REPLICANTON
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November 6, 2003, 23:06:49; Search time 102.25 Seconds (without alignments) 780.185 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                                                                 2141354 seqs, 1595478879 residues
                                                                                                                                                                1 gttcagcttttttgtacaaacttgt 25
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                                                     OM nucleic - nucleic search, using sw model
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Perfect score:
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                                                                                  Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES		Description	Sequence 8, Appli	Sequence 9, Appli	Sequence 4, Appli	Sequence 9, Appli	Sequence 9, Appli	Sequence 49, Appl	Sequence 32, Appl	Sequence 33, Appl	Sequence 44, Appl	Sequence 19, Appl	Sequence 63, Appl					
		ID	US-09-732-914-8	US-09-855-797A-9	US-09-907-900-9	US-09-907-719-9	US-09-432-085-9	US-09-985-448-9	US-10-300-892-9	US-10-055-001A-4	US-10-058-292-9	US-10-162-879-9	US-10-161-403-49	US-10-151-690-32	US-09-974-760B-33	US-09-732-914-44	US-10-151-690-19	US-10-023-208-63
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137, 20, 581, 25,	27.74.4	26, 10, 10,	Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 5, Appl Sequence 10, Appl Sequence 10, Appl Sequence 10, Appl Sequence 50, Appl	44 1
	10-055-001A-K: 10-385-546-7 -10-055-001A-2: -10-055-001A-2:	US-10-055-001A-26 US-10-055-001A-26 US-09-855-797A-10 US-09-907-900-10	US-09-347-119-10 US-09-432-085-10 US-10-300-892-10 US-10-055-001A-5 US-10-058-292-10 US-10-162-879-10 US-10-162-879-10	US-09-732-914-45 US-09-855-797A-42 US-09-907-900-42 US-09-907-719-42 US-09-908-448-42 US-10-300-892-42 US-09-855-797A-15 US-09-907-900-15
2411	12224	44 67	1	9 1 1 2 2 2 2 2 3 3 3 3 3 3 3 3 3 3 3 3 3
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## ALIGNMENTS

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parence 8, Application US/09732914

Patent No. US2002007051A1

GENERAL INFORMATION:

APPLICANT: Cheo, David

APPLICANT: Temple, Gary F.

APPLICANT: Harlie, James L.

APPLICANT: Harlie, James L.

APPLICANT: Harlie, James L.

APPLICANT: Brack, Michael A.

TITLE OF INVENTION: Recombinational Cloning

FILE REFERENCE: 0942.501002

CURRENT APPLICATION NUMBER: US 60/169,983

PRIOR FILING DATE: 2000-12-10

PRIOR FILING DATE: 2000-12-10

PRIOR FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 140

SEQ ID NO 8

LENGTH: 25

LENGTH: 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ch 100.0%; Score 25; DB 9; Length 25; L Similarity 100.0%; Pred. No. 0.3; 25; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TYPE: DNA
; ORGANISM: attR1
US-09-732-914-8
RESULT 1
US-09-732-914-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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GTTCAGCTTTTTTGTACAACTTGT 25 g

1 GITCAGCITITIGIACAACTIGI 25

à

RESULT 2 US-09-855-797A-9 ; Sequence 9, Application US/09855797A

0; Gaps 0; Indels Matches 25; Conservative 0; Mismatches

0;

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Search completed: November 6, 2003, 22:26:28 Job time : 112.5 secs

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Gaps

.. 0 Indels ·, Destination vector pDEST5 nucleotide sequence. Cheo D; Mismatches 4022 GricaGCriririrdiacaaacrigr 3998 25 Temple GF, Example 15; Fig 25; 459pp; English. 1 GTTCAGCTTTTTTGTACAAACTTGT 0; AAC55464 standard; DNA; 5957 BP (LIFE-) LIFE TECHNOLOGIES INC. 99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-2000; 2000WO-US05432. 11-JAN-2001 (first entry) Conservative Brasch MA, Bacteriophage lambda WPI; 2000-543948/49. WO200052027-A1. 28-MAY-1999; 02-MAR-1999; 23-MAR-1999; 08-SEP-2000 25; Hartley JL, AAC55464; Synthetic Matches ð ద

present invention describes isolated nucleic acid molecules (I) Example 15; Fig 26; 459pp; English. AAC55467 RESULT 용 ⋩ The present invention describes isolated nucleic acid molecules (I) concing an attB1, attB2, attP1, attB2, attB1, and attB2 concided an escented mucleic acid molecule (II) comprising one or more att recombination sites comprising one or more mutation in its core region that increases the specificity of interaction between the recombination sites and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at creambination between a first nucleic acid molecule comprising the recombination between a first nucleic acid molecule comprising the comprising a second recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated comprising a second recombination site that interacts with the mutated cart recombination site und a second nucleic acid molecules. They can be used for the recombinational cloning of the present invention are used for the recombinational cloning of cart recombination are used for the recombinational cloning of desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (III), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1 aud attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

ö Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attB2, attL1, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds. Gaps .. Indels 0 Destination vector pDEST6 nucleotide sequence. ά 0; Mismatches Cheo 205 Gricagcririririanacaacrici 181 25 Temple GF, 1 GTTCAGCTTTTTTGTACAAACTTGT AAC55467 standard; DNA; 5957 BP (LIFE-) LIFE TECHNOLOGIES INC. 99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-2000; 2000WO-US05432. (first entry) 25; Conservative Brasch MA, Bacteriophage lambda. WPI; 2000-543948/49. WO200052027-A1. 11-JAN-2001 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; Hartley JL, 08-SEP-2000 AAC55467; Synthetic Matches

Into present. Invention describes isolated mucles action and attR2, and attR2, and attR2, and attR2, and attR2, and attR2, attR2, and attR2, and attR2, and attR2, and attR2, and a second attraction site, and a second attraction site, and attR2, and

1530 A; 1445 C; 1496 G; 1486 T; 0 other; Sequence 5957 BP; DB 21; Length 5957; Score 25; DB 21 Pred. No. 0.48; 100.0%; Query Match Best Local Similarity

DB 21; Length 5957;

100.0%; Score 25; DB 2: 100.0%; Pred. No. 0.48;

Local Similarity

Best

Query Match

Seguence 5957 BP; 1509 A; 1443 C; 1498 G; 1507 T; 0 other;

comprising a second recombination site that interacts with the mutated att recombination site. (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and changing copy (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. 88999999999888

Sequence 4554 BP; 1194 A; 1070 C; 1113 G; 1177 T; 0 other;

Gaps ; 0 Score 25; DB 21; Length 4554; Pred. No. 0.47; 0; Indels 100.0%; bcc. 100.0%; Pred. No. c. 0; Mismatches Query Match
Best Local Similarity 100.
Matches 25; Conservative

25

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310 GricaGCriririridiAchacridr 286 1 GITCAGCTITITIGIACAAACIIGI à

RESULT 37

AAD27063 standard; DNA; 5148 AAD27063/c 

AAD27063;

(first entry) 09-APR-2002

Plasmid pGN39 DNA

construct; RNA inhibition; RNAi; gene expression control; Vector

Unidentified

pGN39 plasmid; ds

WO200188121-A1.

22-NOV-2001

18-MAY-2001; 2001WO-IB01068.

19-MAY-2000; 2000GB-0012233.

(DEVG-) DEVGEN NV

Bogaert Renard J, Plaetinck G,

WPI; 2002-121984/16.

A new DNA vector construct containing opposable promoter and terminator sequences flanking a cloning site are useful for the expression of double stranded RNA useful for inhibition of RNA in gene expression control

Claim 24; Fig 12; 75pp; English.

The present invention relates to improved vector constructs comprising two promoters in opposite orientation to each other, an inter-promoter region downstream of the 3' end of both promoters, a cloning site in the inter-promoter region and a transcription terminator downstream of the 3' end of the first promoter and the cloning site and operably linked to the first promoter. The constructs of the invention and the bacteria harbouring the constructs are used to produce double stranded RNA for RNA inhibition (RNAi) and can be used as a tool for controlling gene expression. The present sequence is pGN39 plasmid DNA

Sequence 5148 BP; 1359 A; 1199 C; 1279 G; 1311 T; 0 other;

100.0%; Score 25; DB 24; Length 5148; 100.0%; Pred. No. 0.47; Best Local Similarity Query Match

0; Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds. Gaps .. 0 Indels ô Destination vector pDEST13 nucleotide sequence. Cheo D; Mismatches 171 Gircascriririgiacaaacrist 147 25 Brasch MA, Temple GF, 0; (LIFE-) LIFE TECHNOLOGIES INC. 99US-0122389. 99US-0126049. 99US-0136744. AAC55481 standard; DNA; 5848 02-MAR-2000; 2000WO-US05432. (first entry) Conservative Bacteriophage lambda 1 GTTCAGCTTT WO200052027-A1. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; Hartley JL, 11-JAN-2001 08-SEP-2000 25; Synthetic RESULT 38 AAC55481/c Matches 셤 ð

encoding an attB1, attB2, attB1, and attB2 nuclecties sequence. Also described att recombination sites or a second att recombination site, and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising a second recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting desired proceins, operably linking nucleic acid molecules, constructing queen proclains, clearing flusion tags from desired proceins, operably linking nucleic acid molecules. changing copy number, changing replicons, cloning into phages and cloning: (1), (11), (111), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. present invention describes isolated nucleic acid molecules (I)

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attL2 nucleotide sequence useful for the recombinational cloning of polypeptides -

WPI; 2000-543948/49

Disclosure, Fig 33; 459pp; English.

Sequence 5848 BP; 1563 A; 1364 C; 1379 G; 1542 T; 0 other;

100.0%; Score 25; DB 21; Length 5848; 100.0%; Pred. No. 0.48; Best Local Similarity Query Match

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recombination in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site. (I), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins,
                                                                                                                                                                                                                                                                                                  changing copy number, changing replicons, cloning into phages and proming. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 420 BP; 134 A; 77 C; 88 G; 121 T; 0 other;
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100.0%; Score 25; DB 21; Length 420; 100.0%; Pred. No. 0.39; 0; Indels 0; Mismatches GTTCAGCTTTTTTGTACAAACTTGT 378 25 1 GTTCAGCTTTTTTGTACAAACTTGT 100.0%; Query Match
Best Local Similarity luv..
Best 25; Conservative ò

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Gaps

. 0

402 g

AAD44626 standard; DNA; 1846 BP. AAD44626, 

AAD44626;

13-DEC-2002 (first entry)

Gateway transfer cassette DNA.

Prokaryotic library; candidate protein; nucleic acid modification; NAM; enzyme attachment sequence; BAS; clinical pharmacology; chemical sensor; enzymology; cosmetic research; toxic; environmental safety assessment; nutrient biology; gateway transfer cassette; gene; ds.

Unidentified

WO200266653-A2

29-AUG-2002.

14-DEC-2001; 2001WO-US49058.

14-DEC-2000; 2000US-256163P.

(XENC-) XENCOR INC.

Liu Y; Li M, WPI; 2002-667068/71.

New library of prokaryotic pET-24a expression vectors, host cells nucleic acid/protein conjugates, useful for screening candidate proteins and their nucleic acids or modification enzymes for pharmacogenetic analysis

or

Example 2; Fig 59B; 127pp; English.

The invention relates to methods and compositions for the construction of prokaryotic libraries expressing candidate proteins and the use of these to identify candidate proteins and the nucleic acids encoding them. The invention provides a library of prokaryotic pET-24 vectors comprising a fusion nucleic acid consisting of a nucleic acid encoding a mucleic acid modification (NAM) enzyme or a candidate protein, or a nucleic acid having a T7 promoter operably linked to the NAM enzyme or the candidate protein, and an enzyme attachment sequence (EAS) recognised by the NAM enzyme. The library is used for identifying

0 The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule candidate proteins and mucleic acids encoding these proteins, in screening for NAM enzymes with decreased toxicity for the host cells, or in identifying novel or improved EASs, which may be used for understanding cellular processes or any subsequent therapeutic or toxic activities. The nucleic acid/protein (NAP) conjugates are useful in diagnostic assays and in research including clinical pharmacology, functional genomics, pharmacogenomics, agricultural chemicals, environmental safety assessment, chemical sensor, nutrient biology, cometic research or enzymology. These may also be used in in vitro screening techniques and in assays with target molecules. The present sequence is gateway transfer cassette DNA used in the invention. attR reading frame C parent plasmid prfC Parent III nucleotide sequence. Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds. Gaps 0; 100.0%; Score 25; DB 24; Length 1846; 100.0%; Pred. No. 0.44; 0; Indels Sequence 1846 BP; 527 A; 381 C; 434 G; 504 T; 0 other; Ď, 0; Mismatches Cheo 1 GITCAGCITITITIGIACAAACTIGI 25 Brasch MA, Temple GF, Example 14; Fig 83; 459pp; English. 25 GTTCAGCTTTTTTGTACAAACTTGT (LIFE-) LIFE TECHNOLOGIES INC AAC55541 standard; DNA; 4554 99US-0122389. 99US-0126049. 02-MAR-2000; 2000WO-US05432. 99US-0136744. (first entry) 25; Conservative Bacteriophage lambda. WPI; 2000-543948/49. Local Similarity WO200052027-A1. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; 11-JAN-2001 Hartley JL, 08-SEP-2000. Synthetic AAC55541; Query Match Matches RESULT 36 AAC55541 à g 8×300000000000×8

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recombination between a first mucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. [1], [11], primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning (1), [11], [11], host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is
               888888888888888888
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Seguence 306 BP; 87 A; 77 C; 80 G; 62 T; 0 other;

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0;
DB 21; Length 306;
0.38;
hes 0; Indels
          100.0%; Prec. ...
  100.0%; Score 25; 100.0%; Pred. No.
                                                                       301 GricaGcrirririciacaaacrici 277
                                                25
                                                  TIGIACAAACIIGI
             Local Similarity 100.
les 25; Conservative
                                                   1 GTTCAGCTTTI
      Query Match
                           Matches
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Gaps

AAC55514/c RESULT 33

AAC55514 standard; DNA; 306

AAC55514;

(first entry) 11-JAN-2001 Destination vector pDEST26 fragment nucleotide sequence.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda

Synthetic

WO200052027-A1.

08-SEP-2000

02-MAR-2000; 2000WO-US05432.

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999;

LIFE-) LIFE TECHNOLOGIES INC

Cheo D; Temple GF, Brasch MA, Hartley JL,

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, a attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -Disclosure; Fig 46; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attB1, attB2 attB1, attB2 attB1, attB2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at 

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2 attB1, attB2 attB1, attB2 attB1, attB2 attB1, attB2 attB2 attB1, and attB2 molecule (II) comprising one more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at

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recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising the comprising a second recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for charging vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning into phages and production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                         100.0%; Score 25; DB 21; Length 306; 100.0%; Pred. No. 0.38; ntive 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Destination vector pDEST18 fragment nucleotide sequence.
                                                                                                                                                                                                                                                            Sequence 306 BP; 84 A; 83 C; 74 G; 65 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cheo
                                                                                                                                                                                                                                                                                                                                                                                 301 GITCAGCITITITIGIACAAACIIGT 277
                                                                                                                                                                                                                                                                                                                                                              1 GIICAGCITITITITITACAACTIGI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Temple GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 38; 459pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC55492 standard; DNA; 420 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LIFE-) LIFE TECHNOLOGIES INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0136744
                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100..
Best 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-543948/49.
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28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        )8-SEP-2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC55492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 34
AAC55492/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGGGGGGGX8X4444X4X4X4X4X4X6X4X8X8X<del>4X4</del>4X4X4X6X6X6
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recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
one mutation in its core region that enhances the efficiency
                 \mathcal{G}_{\mathcal{G}}^{\mathcal{G}}(\mathcal{G}_{\mathcal{G}}) = \mathcal{G}_{\mathcal{G}}^{\mathcal{G}}(\mathcal{G}_{\mathcal{G}}) + \mathcal{G}
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Sequence 255 BP; 88 A; 57 C; 50 G; 60 T; 0 other;

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Gaps
                                    0
100.0%; Score 25; DB 21; Length 255; 100.0%; Pred. No. 0.38;
                                    0; Indels
                  Best Local Similarity 100.0%; Pred. No. 0.3
Matches 25; Conservative 0; Mismatches
                                                                                                        253 Gircagciriririgiacaaacirgi 229
                                                                       25
                                                                         1 GTTCAGCTTTTTTGTACAAACTTGT
     Query Match
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AACSS478 standard; DNA; 255

BP.

AAC55478;

11-JAN-2001 (first entry)

Destination vector pDEST12 fragment nucleotide sequence.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda

Synthetic

WO200052027-A1.

08-SEP-2000

99US-0122389,

02-MAR-2000; 2000WO-US05432.

99US-0126049. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC

Cheo Temple GF, Brasch MA, Hartley JL,

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 15; Fig 32; 459pp; English.

encoding an attB1, attB2, attP1, attB2, attL1, attB2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site, and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at The present invention describes isolated nucleic acid molecules (I) 

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recombination in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the cumprising a second recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
               $XGGGGGGGGGGGGGG
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Sequence 255 BP; 80 A; 67 C; 58 G; 50 T; 0 other;

Gaps .. DB 21; Length 255; 0; Indels 100.0%; Score 25; DB 21 100.0%; Pred. No. 0.38; 0; Mismatches 25; Conservative Query Match Best Local Similarity Matches

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235 Grrcagerrrrrrraracaaacrrer 211 1 GTTCAGCTTTTTTGTACAAACTIGT 25 ò g

AAC55468/c RESULT 32

BP. AAC55468 standard; DNA; 306

AAC55468;

11-JAN-2001 (first entry)

Destination vector pDEST7 fragment nucleotide sequence.

Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda Synthetic

WO200052027-A1.

08-SEP-2000 

02-MAR-2000; 2000WO-US05432.

99US-0122389. 99US-0126049 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC.

Cheo Temple GF, Brasch MA, Hartley JL,

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WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 15; Fig 27; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attL1, attL2, attB2, attB1 mud attB2 muclecide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second attribute comprising comprising one or more mutated att recombination sites comprising at

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recombination in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), primers, vectors and methods att recombination site. (I) (II), primers, vectors and methods incleic acid molecules. They can be used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning; (I), (II), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
                8888888888888888888888888
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Sequence 204 BP; 80 A; 35 C; 31 G; 58 T; 0 other;

Gaps ó Score 25; DB 21; Length 204; Pred. No. 0.37; 0; Indels 0; Mismatches 100.0%; Query Match
Best Local Similarity 100.0° Matches 25; Conservative à

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RESULT 29

AAC55476/c 

AAC55476 standard; DNA; 204 BP AAC55476;

(first entry) 11-JAN-2001 Destination vector pDEST11 fragment nucleotide sequence.

Bacteriophage lambda; att; recombination site; attB; attP; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda

Synthetic

WO200052027-A1.

02-MAR-2000; 2000WO-US05432. 08-SEP-2000

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC.

Temple GF, Brasch MA, Hartley JL,

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 13; Fig 31; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2 attB1, attB2 attB1, attB2 attB1, and attR2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site, and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2 attB1, attB2 attB1, attB2 
Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the

recombinational cloning of polypeptides -

WPI; 2000-543948/49.

Disclosure; Fig 24; 459pp; English.

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least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising the comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning: (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                     ö
                                                                                                                                                                                                                                                                   100.0%; Score 25; DB 21; Length 204; 100.0%; Pred. No. 0.37; cive 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        His6-Trx expression cassette for destination vector pDEST4.
                                                                                                                                                                                                                                         Sequence 204 BP; 60 A; 53 C; 50 G; 41 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       á
                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheo
                                                                                                                                                                                                                                                                                                                                                     181 GTTCAGCTTTTTTGTACAAACTTGT 157
                                                                                                                                                                                                                                                                                                                                   1 GTTCAGCTTTTTGTACAAACTTGT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Temple GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                               BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LIFE-) LIFE TECHNOLOGIES INC.
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99US-0126049.
99US-0136744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32-MAR-2000; 2000WO-US05432.
                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC55460 standard; DNA; 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                     25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteriophage lambda.
                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200052027-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAC55460;
                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 30
                                                                                                                                                                                                                                                                                                                                                                                                                                AAC55460/
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recombination in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site in [III], primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from cepulated protects, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 153 BP; 50 A; 28 C; 40 G; 35 T; 0 other;
                       $$$$$$$$$$$$$$$$$$$$$$$
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Gaps
                                     0
100.0%; Score 25; DB 21; Length 153; 100.0%; Pred. No. 0.37; ive 0; Mismatches 0; Indels C
                                                                                                   127 GrickGcriririchacaacricr 103
                                                                     1 GITCAGCITITITIGIACAAACIIGI 25
                                        25; Conservative
                         Local Similarity
        Query Match
                                           Matches
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AAC55465 standard; DNA; 204 BP AAC55465; 

(first entry) 11-JAN-2001

Destination vector pDEST6 fragment nucleotide sequence #1.

Bacteriophage lambda; att; recombination site; attB; attR; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda Synthetic

WO200052027-A1

08-SEP-2000

02-MAR-2000; 2000WO-US05432.

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; TIFE-) LIFE TECHNOLOGIES INC

Cheo Temple GF, Brasch MA, Hartley JL,

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WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -The present invention describes isolated nucleic acid molecules (I) Example 15; Fig 26; 459pp; English.

nucleotide an attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2, at

recombination in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from cegulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning: (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. 

Sequence 204 BP; 70 A; 40 C; 46 G; 48 T; 0 other;

Gaps .. 100.0%; Score 25; DB 21; Length 204; 100.0%; Pred. No. 0.37; 0.37; 0; Indels 0; Mismatches Query Match
Best Local Similarity 100.
Matches 25; Conservative

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В  $\delta$ 

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RESULT 28 AAC55470/c

AAC55470 standard; DNA; 204

AAC55470;

(first entry) 11-JAN-2001 Destination vector pDEST8 fragment nucleotide sequence.

Bacteriophage lambda; att; recombination site, attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda. Synthetic

WO200052027-A1.

08-SEP-2000,

99US-0126049. 02-MAR-2000; 2000WO-US05432 99US-0122389 02-MAR-1999; 23-MAR-1999; 

TECHNOLOGIES INC. (LIFE-) LIFE 28-MAY-1999;

Cheo Temple GF, Brasch MA, Hartley JL,

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WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, a attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 15; Fig 28; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attB1, attB2, attB1, attB2 attB1, attB2 attB1, attB2 attB1, attB2 attB1, attB2 attB1 and attB2 muclecide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at

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recombination in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (1), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting ene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory generals sequences, constructing genes for fusion proteins,
                                                                                                                                                                                                                                                                                                                      changing copy number, changing replicons, cioning into phages and cloning. (I), (II), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 125 BP; 61 A; 18 C; 14 G; 32 T; 0 other;
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100.0%; Score 25; DB 21; Length 125; 100.0%; Pred. No. 0.36; tive 0; Mismatches 0; Indels ( 1 GITCAGCITITITGIACAAACTIGI 25 25 Gricagcriririrgiacaacrigi 1 Query Match
Best Local Similarity lov...
best Local 25; Conservative

ò g

AAC55485 standard; DNA; 153 BP RESULT 25 AAC55485,

AAC55485; 

(first entry) 11-JAN-2001 Destination vector pDEST15 fragment nucleotide sequence #2.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda Synthetic

WO200052027-A1.

08-SEP-2000

02-MAR-2000; 2000WO-US05432.

99US-0136744. 99US-0122389. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC

Cheo Temple GF, Brasch MA, Hartley JL,

WPI; 2000-543948/49.

attP2, Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1 and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides  $^{-}$ 

Disclosure; Fig 35; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB2, attB1, attB2, attB1, attB2, attB1, attB2 attB1, attB2 attB2, and attB2 nucleide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at

least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (1), (11), (111), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting easier products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing replicons, cloning into phages and cloning. (1), (11), (111), host cells and vectors can be used in the exemplification of the present invention. 

Sequence 153 BP; 52 A; 29 C; 33 G; 39 T; 0 other;

Gaps ., 100.0%; Score 25; DB 21; Length 153; 100.0%; Pred. No. 0.37; cive 0; Mismatches 0; Indels ( Best Local Similarity 100.0%;
Matches 25; Conservative 0 Query Match

; 0

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·;

Gaps

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RESULT 26 AAC55488/

BP AAC55488 standard; DNA; 153

AAC55488;

11-JAN-2001 (first entry)

Destination vector pDEST16 fragment nucleotide sequence #2.

Bacteriophage lambda; att; recombination site; attB; attR; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda

Synthetic

WO200052027-A1.

08-SEP-2000

99US-0122389. 02-MAR-2000; 2000WO-US05432 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; 

(LIFE-) LIFE TECHNOLOGIES INC.

99US-0126049.

Cheo Temple GF, Brasch MA, Hartley JL,

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WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Disclosure, Fig 36; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site, and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at

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mutated att recombination site and a second mutated acid molecule comprising a second recombination site that interacts with the mutated tr recombination site. (1), (11), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting quene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and changing copy number, changing replicons, cloning into phages and production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the
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Seguence 102 BP; 37 A; 24 C; 19 G; 21 T; 1 other;

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0
                                   Gaps
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   100.0%; Score 25; DB 21; Length 102; 100.0%; Pred. No. 0.35; 1. Indels ive 0; Mismatches 0; Indels
Query Match
Best Local Similarity 100.0%; Pred. No. 0.3:
Matches 25; Conservative 0; Mismatches
                                                                   GITCAGCITITITIGIACAACTIGI 25
                                                                                   92 GTTCAGCTTTTTTGTACAAACTTGT 68
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AAC55453 standard; DNA; 120 RESULT 23

ВР

(first entry) 11-JAN-2001 AAC55453;

Trc expression cassette for destination vector pDEST1.

Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda. Escherichia coli.

WO200052027-A1.

08-SEP-2000

2000WO-US05432. 02-MAR-2000; 99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC.

Cheo D; Brasch MA, Temple GF, Hartley JL,

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Disclosure; Fig 21; 459pp; English.

encoding an attB1, attB2, attP1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) present invention describes isolated nucleic acid molecules (I) rhe 

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site (II), (III), primers, vectors and methods att recombination are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to requiatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning into (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is \$

Sequence 120 BP; 44 A; 19 C; 28 G; 29 T; 0 other;

Gaps 0 100.0%; Score 25; DB 21; Length 120; 0; Indels 0.36; Mismatches Pred. No ;0 100.0%; Conservative Local Similarity les 25; Conserv Query Match Matches

; 0

ò g RESULT 24 AAC55384,

AAC55384 standard; DNA; 125

ВР

AAC55384;

(first entry) 11-JAN-2001 Recombination site nucleotide sequence attR1.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; mutant, recombinational cloning, entry vector; d gene product targeting; fusion tag cleavage; ds.

WO200052027-A1.

Bacteriophage lambda.

08-SEP-2000 

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-2000; 2000WO-US05432 02-MAR-1999; 23-MAR-1999; 28-MAY-1999;

(LIFE-) LIFE TECHNOLOGIES INC.

Cheo Temple GF, Brasch MA, Hartley JL,

Ü,

WPI; 2000-543948/49.

attP2, Isolated nucleic acid molecules encoding an attB1, attB2, attP1, a attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Claim 1; Fig 9; 459pp; English.

encoding an attB1, attB2, attP1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at The present invention describes isolated nucleic acid molecules (I)

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comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (1), (11), (111), primers, vectors and methods care from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning (1), (11), (111), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 102 BP; 40 A; 22 C; 18 G; 22 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTICAGCTTTTTTGTACAACTTGT 59
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AACS5508 standard; DNA; 102 AAC55508; 

BP

(first entry) 11-JAN-2001 Destination vector pDEST24 fragment nucleotide sequence #1.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda

WO200052027-A1.

08-SEP-2000

02-MAR-2000; 2000WO-US05432.

99US-0122389.

99US-0136744 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC

Cheo D; Temple GF, Hartley JL, Brasch MA,

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1 and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 5; Fig 44; 459pp; English.

encoding an attB1, attB2, attB1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site, and (2) an isolated nucleic acid molecule (III) present invention describes isolated nucleic acid molecules (I)

encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site, and (2) an isolated nucleic acid molecule (III)

The present invention describes isolated nucleic acid molecules (I)

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least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the comprising a second bracion site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, rargeting gene products to intracellular locations, cleaving fusion tags from regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning: (I), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage lambda; att; recombination site; attB; attB; attL; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
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or more mutated att recombination sites comprising at
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                                                                                                                                                                                                                                                                                              100.0%; Score 25; DB 21; Length 102; 100.0%; Pred. No. 0.35; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Destination vector pDEST25 fragment nucleotide sequence #1.
                                                                                                                                                                                                                                                                      Sequence 102 BP; 37 A; 25 C; 19 G; 21 T; 0 other;
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                                                                                                                                                                                                                                                                                                                     Local Similarity 100.0%; Pred. No. 0.3 (es 25; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Fig 45; 459pp; English.
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99US-0126049.
99US-0136744.
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23-MAR-1999;
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comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site in the tinteracts with the mutated att recombination site. [1], [11], [11], primers, vectors and methods trom the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, leaving fusion tages from cestived proteins, operably linking mucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and changing (i) (III), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. 8×333333333333333333

Sequence 102 BP; 35 A; 19 C; 20 G; 28 T; 0 other;

0 100.0%; Score 25; DB 21; Length 102; 100.0%; Pred. No. 0.35; 0; Indels 100.0%; Pred. No. 1 GITCAGCITITITGIACAAACTIGT 25 70 Gricagciriritaracaacirica 46 25; Conservative Query Match Best Local Similarity Matches ઠે g

AAC55500 standard; DNA; 102 BP

AAC55500;

(first entry) 11-JAN-2001 Destination vector pDEST21 fragment nucleotide sequence #2.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda Synthetic

WO200052027-A1

08-SEP-2000

02-MAR-2000; 2000WO-US05432.

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC

Cheo

Brasch MA, Temple GF,

Hartley JL,

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nuclectide sequence useful for the recombinational cloning of polypeptides -WPI; 2000-543948/49.

Disclosure; Fig 41; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attB1, attB2, attB1, and attR2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more attrecombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second attrecombination site; and (2) an isolated nucleic acid molecule (III) 

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated comprising a second recombination site that interacts with the mutated att recombination site. (1), (11), (11), (11), vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from genie proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (1), (11), (111), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. \$

Sequence 102 BP; 45 A; 13 C; 24 G; 20 T; 0 other;

Gaps · 0 100.0%; Score 25; DB 21; Length 102; 100.0%; Pred. No. 0.35; 0; Indels Mismatches 100.08; 22. Conservative l Similarity 25; Conserv Query Match Best Local Matches

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Gaps

RESULT 20 AAC55505/

品 AAC55505 standard; DNA; 102

AAC55505;

(first entry) 11-JAN-2001 

Destination vector pDEST23 fragment nucleotide sequence #1.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda. Synthetic

WO200052027-A1

08-SEP-2000

02-MAR-2000; 2000WO-US05432

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; TECHNOLOGIES INC (LIFE-) LIFE

Temple GF, Brasch MA, Hartley JL,

Ċ,

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Example 5; Fig 43; 459pp; English.

The present invention describes isolated nucleic acid molecules (1) encoding an attB1, attB2, attB1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site, and (2) an isolated nucleic acid molecule (III)

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comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. [1], (II), (III), primers, vectors and methods att recombination are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Destination vector pDEST20 fragment nucleotide sequence #2.
                                                                                                                                                                                                                                                                                                                                                     Score 25; DB 21; Length 87;
Pred. No. 0.35;
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                                                                                                                                                                                                                                                                                                                  Sequence 87 BP; 26 A; 19 C; 21 G; 21 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
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99US-0126049.
99US-0136744.
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Best Local Similarity 100.0
Matches 25; Conservative
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23-MAR-1999;
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comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated comprising a second recombination site (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracelular locations, cleaving fusion tags from the present contracelular locations, cleaving fusion tags from regulatory genetic sequences, constructing genes for fusion proteins, changing replicons, cloning into phages and claning (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more attraccombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second attraccombination site; and (2) an isolated nucleic acid molecule (III)
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one or more mutated att recombination sites comprising at
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0
                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 25; DB 21; Length 95; 100.0%; Pred. No. 0.35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GST expression cassette for destination vector pDEST3 #2.
                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                                                                                                               Sequence 95 BP; 41 A; 13 C; 15 G; 26 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ů,
                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 100.0%; Pred. No. 0.3
Matches 25; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheo
                                                                                                                                                                                                                                                                                                                                                                                                                                    25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 15; Fig 23; 459pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52 gricagcriririrgiacaaacrigi
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GITCAGCITITITGIACAACTIGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0122389.
99US-0126049.
99US-0136744.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 02-MAR-2000; 2000WO-US05432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC55458 standard; DNA; 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage lambda.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-543948/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VO200052027-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-MAR-1999;
23-MAR-1999;
28-MAY-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            38-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC55458;
                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC55458/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8
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ó

Gaps ; 0

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AASO6174-AASO6322 represent Bacteriophage lambda att recombination site nucleic acid sequences, and PCR primers of the invention. The att sequences are recognised by the recombination protein lambda att sequences are recognised by the recombination protein lambda integrase (Int). The invention is a new method of producing a population of hybrid nucleic acids comprising mixing at least a first population of nucleic acids comprising one or more recombination sites with at least causing some or all of the nucleic acids to recombine with all or some of the target nucleic acids acids to recombine with all or some of the target nucleic acids to see as an or accombine with all or some of the target nucleic acids which may be the same or different. The nucleic acids may be used to express therapeutic proteins by expressing different sequences like to each other. The method allows simultaneous cloning of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 43 BP; 20 A; 5 C; 11 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                 two or more different nucleic acids.
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100.0%; Score 25; DB 22; Length 43; 100.0%; Pred. No. 0.33; ive 0; Mismatches 0; Indels 1 GIICAGCITITITGIACAAACTIGI 25 29 GricaGCririridaAcaactigi 5 Local Similarity 100. es 25; Conservative Query Match Matches

AACSSS03 standard; DNA; 82 RESULT 15

ద à

BP

AAC55503;

11-JAN-2001 (first entry)

Destination vector pDEST22 fragment nucleotide sequence #2.

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda Synthetic

WO200052027-A1

08-SEP-2000

02-MAR-2000; 2000WO-US05432.

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999;

(LIFE-) LIFE TECHNOLOGIES INC

Cheo

Temple GF,

Brasch MA,

Hartley JL,

WPI; 2000-543948/49.

attP1, attP2, for the isolated nucleic acid molecules encoding an attB1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence useful attii, attii, attki, and attki nucleotid recombinational cloning of polypeptides

Disclosure, Fig 42; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attB1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (I) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) 

comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site and a second nucleic acid molecule.

Tre comprising a second recombination site that interacts with the mutated att recombination site. [1], [11], [11], primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from esquatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning (0) [11], [11], host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention. 55555555555555555X8

Sequence 82 BP; 39 A; 16 C; 17 G; 10 T; 0 other;

Gaps 0 100.0%; Score 25; DB 21; Length 82; 100.0%; Pred. No. 0.35; 0; Indels 0; Mismatches 100.0%; 1 Similarity 100. 25; Conservative Query Match Local Matches Best

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gg

ð

Gaps . 0

RESULT 16

BP AAC55517 standard; DNA; 87

AAC55517;

Destination vector pDEST27 fragment nucleotide sequence #2. (first entry) 11-JAN-2001 

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; ds.

Bacteriophage lambda Synthetic

WO200052027-A1.

08-SEP-2000.

02-MAR-2000; 2000WO-US05432

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999;

TECHNOLOGIES INC (LIFE-) LIFE Cheo D; Temple GF, Brasch MA, Hartley JL,

MPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, a attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Disclosure; Fig 47; 459pp; English.

encoding an attB1, attB2, attB1, attB2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site, and (2) an isolated nucleic acid molecule (III) present invention describes isolated nucleic acid molecules (I)

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merabolite by a rungues. This involves modulating the expression of at least one ZBC (zinc binuclear duster protein) gene in a manner to improve the yield of the secondary metabolite. Methods of the invention may be used for improving the production of the secondary metabolite e.g. antibacterial (such as beta-lactam), an anti-hypercholesterolaemic (such as lowastin or mevastatin), an immunosuppressant (such as cyalicin), a glucan synthase inhibitor; gliotoxin family of compounds, a fungal toxin, a modulator of cell surface receptor signalling, a plant growth regulator, a pigment, an insecticide, or an antineoplastic compound. The method results in a decrease in fermentor run-time, a decrease in the size of the fermentor required for the production of equivalent amounts of the secondary metabolite, or a decrease in the biase of the fermentor required for the production of equivalent amounts of the secondary metabolite, or a decrease in the biases required for the production, which translates into decreased waste that must be handled in downstream processing. The sequences given in records ABISSSS7ABISSSS represent primers that are used in construction of vectors containing the ZBC genes of the invention.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained directly from WIPO at
metabolite by a fungus. This involves modulating the expression of at least one ZBC (zinc binuclear cluster protein) gene in a manner to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 35 BP; 14 A; 7 C; 7 G; 7 T; 0 other;
       8499999999999999999
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Query Match

100.0%; Score 25; DB 24; Length 35; 100.0%; Pred. No. 0.33; tive 0; Mismatches 0; Indels 1 GTTCAGCTTTTTTGTACAAGCTTGT 25 GTTCAGCTTTTTTGTACAAACTTGT 11 Local Similarity 100. ses 25; Conservative Matches à 셤

; 0

Gaps

; 0

AAC55545 standard; DNA; '43 AAC55545; RESULT 13

11-JAN-2001 (first entry) att site PCR primer attRl 

Bacteriophage lambda; att; recombination site; attB; attB; attL; mutant; recombinational cloning; entry vector; destination vector; gene product targeting; fusion tag cleavage; PCR primer; ss. Bacteriophage lambda; mutant; recombinationa

Bacteriophage lambda Synthetic

40200052027-A1.

38-SEP-2000

02-MAR-2000; 2000WO-US05432.

99US-0122389. 99US-0126049. 99US-0136744. 02-MAR-1999; 23-MAR-1999; 28-MAY-1999; (LIFE-) LIFE TECHNOLOGIES INC

Cheo D; Hartley JL, Brasch MA, Temple GF,

WPI; 2000-543948/49.

Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides -

Producing hybrid nucleic acids, useful for expressing novel therapeutic polypeptides, by mixing the same or different nucleic acids having one or more recombination sites in the presence of recombination proteins,

Example 7; Page 209; 357pp; English.

Byrd DRN;

Hartley JL,

Temple GF,

Brasch MA,

cheo D,

WPI; 2001-356174/37

Example 19; Page 142; 459pp; English.

The present invention describes isolated nucleic acid molecules (I) encoding an attB1, attB2, attP1, attP2, attR1

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nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination sites and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising the mutated att recombination site. (1), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting ene products to intracellular locations, cleaving fusion tags from the present intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing replicons, cloning into phages and cloning (1), (II), (III), host cells and vectors can be used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage lambda; recombination; att site; PCR primer; lambda Int; lambda integrase; therapeutic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR primer attR1 used to produce a population of hybrid DNA molecules.
                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 21; Length 43; 100.0%; Pred. No. 0.33;
                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                    Sequence 43 BP; 20 A; 5 C; 11 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GIICAGCITITITGIACAACTIGI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 GTTCAGCTTTTTGTACAAACTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAS06217 standard; DNA; 43 BP
                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 100.0%;
Matches 25; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-DEC-2000; 2000WO-US33546,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-DEC-1999; 99US-0169983.
09-MAR-2000; 2000US-0188020.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BRASCH M A.
TEMPLE G F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HARTLEY J L
BYRD D R N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHEO D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          #0200142509-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               L2-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAS06217;
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (BRAS/)
(TEMP/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHEO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BYRD/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAS06217
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Disclosure; Page 262; 269pp; English 

The invention relates to a novel method for producing plant artificial chromosomes. The invention also relates to methods for targeting chromosomes. The invention also relates to methods for targeting chromosomes. The thromosomes to selected cells and thromosome, methods for delivery of plant chromosome (PAC) is useful for producing a isolated plant artificial chromosome (PAC) is useful for producing a transgenic plant, which involves introducing the PAC into a plant cell. The PAC comprises a heterologous nucleic acid encoding a gene product such as enzymes, antisense RNA, ENNA, structural proteins, marker proteins, ligands, receptors, ribozymes, therapeutic proteins, and compressed in proteins, and decreased acid actors, antigens, hord factors, antigens, hord factors, antigens, hord factors, antigens, normones, cresistance to diseases, insects, herbicides, or stress in a plant. The resistance to diseases, insects, herbicides, or stress in a plant. The agronomically important trait in the plant, e.g. a product that alters contrined such and/or improves the nutrient quality of the plant. The chromosome (BAC) or a yeast artificial chromosome (YAC). This chromosome (PAC) or a yeast artificial chromosome (YAC). This producing plant artificial chromosomes of the invention.

Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

; Length 25; Indels ; 0 100.0%; Score 25; DB 25; 100.0%; Pred. No. 0.32; 100.0%; Preu. 25; Conservative Best Local Similarity Query Match Matches

25 1 GTTCAGCTTTTTTGTACAACTTGT 25 Grrcherring

> à 임

8- 3-48

AAH19591 standard; DNA; 35 BP.

AAH19591;

(first entry) 30-JUL-2001 Plasmid pEZC7201 ccdB cassette PCR oligo MO511.

Secondary metabolite production; gene expression modulation; genetically modified fungus; antibacterial; antihypercholesterolaemic; immunosuppressant; cell surface receptor signalling; pigment; plant growth regulator; insecticide; anti-neoplastic; ccdB; death gene; pEZC7201; PCR primer; ss 

Unidentified

WO200129073-A1

26-APR-2001

18-OCT-2000; 2000WO-US28903.

20-OCT-1999; 99US-0160587. 19-JAN-2000; 2000US-0487558.

(MICR-) MICROBIA INC

Maxon M; Madden K, , Silva J; Hecht P, Holtzman D, M., Salama S, Sherman A, a M, Feibelman T; Busby R, Doten R, Cali B, Hech Milne T, Norman T, Royer J, Sa Summers E, Zhang L, Mayorga M,

WPI; 2001-374304/39.

Improving production of secondary metabolite by fungus, for producing proteins of interest, involves modulating the expression of gene involved in regulation of secondary metabolite production

Example 1; Page 67; 139pp; English

The present sequence is a primer which was used in an example illustrating an invention relating to a method for improving production of a secondary metabolite by a fungus. The method involves modulating the expression of a gene involved in the regulation of secondary metabolite production. The gene may be modulated in a manner that increases the yield or productivity of metabolite, increases the yield or productivity of metabolite, increases (see felux or excretion of the metabolite, decreases production of side effects or competing metabolites, alters the characteristics of the fungus in a manner that is beneficial to the production of the metabolite, causes conditional lysis of the fungus, or increases the resistance of the fungus to deleterious effects of exposure to the secondary metabolite. The method is useful for producing secondary metabolites such as antibacterial compounds, conditional tentorial compounds, condary metabolites such as antibacterial compounds. antihypercholesterolaemic compounds, immunosuppressants, modulators of cell surface receptor signalling, plant growth regulators, pigments, insecticides or anti-neoplastic compounds. The present sequence was production in the preparation of clones to regulate secondary metabolite production used X2222222222

Sequence 35 BP; 14 A; 7 C; 7 G; 7 T; 0 other;

Gaps 0; 100.0%; Score 25; DB 22; Length 35; 100.0%; Pred. No. 0.33; Indels . 0 0; Mismatches 25; Conservative Best Local Similarity Query Match Matches

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ö g

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Gaps

RESULT 12

BP. ABL58593 standard; DNA; 35 ABL58593/

ABL58593;

(first entry) 24-JUL-2002

Oligonucleotide MO511.

Secondary metabolite; fungus; ZBC gene; zinc binuclear cluster protein; antibacterial; beta-lactam; anti-hypercholesterolaemic; lovastin; mevastatin; immunosuppressant; cyclosporin A; ergot alkaloid; ergotamine; angiogenesis inhibitor; ovalicin; glucan synthase inhibitor; gliotoxin; fungal toxin; cell surface receptor; plant growth regulator; pigment; insecticide; antineoplastic; PCR; primer; ss.

WO200224865-A2. 

28-MAR-2002

19-SEP-2001; 2001WO-US29288

19-SEP-2000; 2000US-233564P

(MICR-) MICROBIA INC.

Sherman A; Maxon M, Madden K, Holtzman D,

WPI; 2002-352005/38.

New method for improving the production of a secondary metabolite e.g. antineoplastic agent, ergot alkaloid from a fungus involves modulation of the expression of at least one zinc binuclear cluster protein gene

Example 1; SEQ ID 7; 49pp + sequence listing; English

The invention relates to improving the production of a secondary

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Nucleic acid insertion, recombination, nucleic acid selection, nucleic acid isolation, att, ds.
                                                                                                                                                                                                                                                                                  GTTCAGCTTTTTTTGTACAACTTGT 25
                                                                                                                                                                                                                                                                                              GIICAGCIIITITIGIACAAACIIGI 25
                   CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
                                                                                                                                                                                                                                                                                                                                                                    Att site nucleotide sequence attR1
                                                                                                                                                                                                                                                                                                                                                                                                                                            21-MAY-2002; 2002WO-US15947.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-MAY-2001; 2001US-291973P.
30-MAY-2001; 2001US-294758P.
21-MAR-2002; 2002US-366891P.
                                                                                                                                                                                                                                                                                                                               ABZ58734 standard; DNA; 25
                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 100...
Best Local 25; Conservative
                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (INVI-) INVITROGEN CORP.
                                                  WPI; 2003-140461/13
                                                                                                                                                                                                                                                                                                                                                                                                                  WO200295055-A2.
                                                                                                                                                                                                                                                                                                                                                        01-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                                                               28-NOV-2002
                               Perkins E,
Stewart S,
                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                            ABZ58734;
                                                                                                                                                                                                                                                                                   Н
                                                                                 interest
                                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                                                                                                                                         ABZ58734
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Gaps

0;

Indels

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0; Mismatches

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The present invention describes a eukaryotic chromosome (I) comprising one or several att sites, where an att site is heterologous to the chromosome, and permits site-directed integration in the presence of chromosome. CC chromosome, and permits site-directed integration in the presence of lambda-integrase. Also described: (I) a platform artificial chromosome expression system (ACCS) (II) comprising several sites that participate in recombinase crallysed recombination; and (2) a method (MI) for introducing a heterologous nucleic acid into a platform artificial chromosome. (I) can be used in gene therapy. (MI) is useful for chromosome, preferably an ACCS. (II) is useful for producing a ratificial chromosome, preferably an ACCS. (II) is useful for producing cranical chromosome, speterably an ACCS. (II) is useful for producing cranical chromosome, microcinlediction, ilpid-mediated transfection, marmal) by introducing (II) by cell fusion, lipid-mediated transfection, microprojectile bombardment or direct DNA transfer into an embryonic cell, preferably a stem cell or an embryo. (II) comprises a heterologous nucleic acid that encodes a therapeutic product which is useful for making a library of ACCS comprising random portions of a genome. ACC44612 cto ACC44732 and ABP95650 to ABP95657 represent sequences used in the exemplification of the present invention.
                                                                                                                                                                                                                                                 Novel eukaryotic chromosome comprising one or many att sites which permits site-directed integration in the presence of lambda-integrase, useful for site-specific recombination-directed integration of DNA of
Ä
Fleming
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 25; DB 25; Length 25; 100.0%; Pred. No. 0.32;
Leung J,
Greene A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Seguence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
Lindenbaum M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 43; Page 143; 272pp; English.
Perez C, L
Shellard J;
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The invention relates to inserting a population of nucleic acids into a second target molecule. The method involves (a) mixing a first population of nucleic acid comprising one or more recombination sites with a target nucleic acid, (b) causing some or all of the nucleic acid molecules of the first population to recombine with the first earget nucleic acid molecules of nucleic acid with a second population; (c) mixing the second population of nucleic acid with a second target nucleic acid, and (d) causing some or all of the nucleic acid molecules of the second population to recombine with some or all of the second target nucleic acid molecules to form a third population of nucleic acid. The method is useful for

selecting and isolating nucleic acid molecules. Sequences ABZ58727-762 represent att recombination site sequences used in the method of the

Inserting a population of nucleic acids into a second target molecule for selecting and isolating nucleic acid molecules by mixing the second population of nucleic acid with a second target nucleic acid -

Disclosure, Fig 13A; 273pp; English.

Byrd DRN;

Esposito D,

Li X,

Cheo D,

Brasch MA,

WPI; 2003-129436/12

o;

Gaps

. 0

0

Length 25; Indels

100.0%; Score 25; DB 25; 100.0%; Pred. No. 0.32;

0; Mismatches

Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;

invention

Query Match

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Producing artificial chromosome by introducing a nucleic acid into plant cell, selecting artificial chromosome that has one or more repeat regions with equivalent amounts of euchromatic and heterochromatic nucleic acids
                                                                                                                                                                                                                                 Plant artificial chromosome; PAC; transgenic plant; vaccine;
blood factor; herbicide; stress; agronomical; nutrient quality;
bacterial artificial chromosome; BAC; yeast artificial chromosome; YAC;
                                                                                                                                                                                                           Artificial plant chromosome related oligo SEQ ID No 40.
                                                                                                                                                                                                                                                                                                                                                                                                                                            CHROMOS MOLECULAR SYSTEMS INC. AGRISOMA INC.
                                    1 GTTCAGCTTTTTTGTACAAACTTGT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       <u>ы</u>
                                                      1 GTTCAGCTTTTTGTACAAACTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perkins
                                                                                                                                BP.
                                                                                                                                                                                                                                                                                                                                                                                                         30-MAY-2001; 2001US-294687P.
04-JUN-2001; 2001US-296329P.
                                                                                                                                                                                                                                                                                                                                                                                30-MAY-2002; 2002WO-US17451
                                                                                                                                ABT16628 standard; DNA; 25
                                                                                                                                                                                  (first entry)
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Perez C, Fabijanski SF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPI; 2003-140436/13
                                                                                                                                                                                                                                                                                                                               WO200296923-A1
                                                                                                                                                                                                                                                                                                    Unidentified
                                                                                                                                                                                                                                                                                                                                                        05-DEC-2002.
                                                                                                                                                                                  03-APR-2003
                                                                                                                                                        ABT16628;
                                                                                                                                                                                                                                                                                                                                                                                                                                               CHRO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AGRI-)
                                                                                                      RESULT 10
                                                                                                                    ABT16628
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The present invention describes a vector (I) comprising operably linked DNA fragments having: (a) origin of replication allowing replication in a recipient cell, preferably in bacteria such as Bacherichia coli; (b) selectable marker region capable of being expressed in the recipient cell; and (c) a chimeric DNA construct comprising: (i) promoter or promoter region capable of being recognized by RNA polymerases of a cukaryotic cell or by prokaryotic RNA polymerase; (ii) first, second, third and fourth recombination sites; (iii) 3' transcription terminating and polyadenylation region functional in the eukaryotic cell. The first and fourth recombination sites, or the second and third recombination sites are capable of reacting with a same recombination site, and preferably are identical. The first and second recombination sites, or the third and fourth recombination sites in our recombination site, or the third and fourth recombination site. The vector is useful for producing large amounts of double-stranded RNA which can be used for allending target mucleic acid sequences. The vectors can also be used to convert a DNA fragment into an inverted repeat structure. Plants transformed with a vector from the present invention can be used in a convertional breeding scheme to produce more plants with the same characteristics or to introduce a chimeric gene for reduction of the present sequence represents expression of nucleic acids. The present sequence represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chromosome-based platform, artificial chromosome; eukaryotic chromosome; att site; integrase; recombinase; ACes; gene therapy; transgenic animal; platform artificial chromosome expression system; PCR primer; ss.
                                                                                                                                                                                           New vectors comprising operably linked DNA fragments having an origin of replication, a selectable marker and a chimeric DNA construct, useful for silencing target nucleic acids and for producing large amounts of double-stranded RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 25; DB 24; Length 25; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Recombination site related oligonucleotide SEQ ID NO:49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Prec. ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        exemplification of the present invention.
                                                                (CSIR ) COMMONWEALTH SCI & IND RES ORG.
                                                                                                           Helliwell C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GTTCAGCTTTTTTGTACAACTTGT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GITCAGCITITITITIONAACTIGT 25
                                                                                                                                                                                                                                                                                                            Disclosure; Page 14; 104pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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  26-JAN-2001; 2001US-264067P. 29-NOV-2001; 2001US-333743P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACC44658 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25; Conservative
                                                                                                             Waterhouse P,
                                                                                                                                                    WPI; 2002-682669/73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200297059-A2
                                                                                                           Wesley S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
ACC44658
  à
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         임
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an isolated nucleic acid molecule (I) comprising a first nucleic acid sequence having a defined sequence (AAC87866 to AAC87881, sequences complementary to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87881, or an RNA sequence corresponding to AAC87866 to AAC87881. Also described are: (1) an isolated nucleic acid molecule (II) comprising a first mutated recombination site that removes one or more stop codons from the recombination site of a size and isolated nucleic acid molecule (III) comprising a first att recombination site comprising a mutation that comprising a first att recombination site comprising a mutation that above mentioned nucleic acids; and (4) cells comprising the above mentioned nucleic acids or (IV). The nucleic acids are used in mutative sites suitable for subcloning reactions in vito or in vivo makes the methods for Data RNA subcloning, highly specific, rapid, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                Isolated nucleic acid molecules comprising a DNA segment having two engineered recombination sites, derived from att or lox, which flank a selectable marker and comprise a core region having an engineered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chimeric nucleic acid construct; recombinational cloning; silencing; recombination site; double stranded RNA; plant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22; Length 25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Core sequence of recombination site attR1 SEQ ID NO:4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 25; DB 22
100.0%; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTTCAGCTTTTTTGTACAAACTTGT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Column 18; 73pp; English.
                                                                                                                                                                                                                     (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                           96US-0663002.
98US-0005476.
95US-0486139.
                                                                                    99US-0233493.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABQ82121 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 100.
Matches 25; Conservative
                                                                                                                                                                                                                                                              Brasch MA, Hartley JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             less labour intensive
                                                                                                                                                                                                                                                                                                         WPI; 2001-049004/06.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200259294-A1
                                                                                       20-JAN-1999;
                                                                                                                                07-JUN-1996;
                                                                                                                                                    L2-JAN-1998;
                                                                                                                                                                         07-JUN-1995;
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US6143557-A.
                                           07-NOV-2000
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AASO6174-AASO6322 represent Bacteriophage lambda att recombination attenucleic acid sequences, and PCR primers of the invention. The att sequences are recognised by the recombination protein lambda integrase (Int). The invention is a new method of producing a population of hybrid nucleic acids comprising mixing at least a first population of nucleic acids comprising one or more recombination sites with at least one target nucleic acids comprising one or more recombination sites and causing some or all of the nucleic acids to recombine with all or some of the target nucleic acids which may be the same or different. The nucleic acids which may be the same or different. The nucleic may also be used to express therapeutic proteins or peptides and they may also be used to cach other. The method allows simultaneous cloning of two or more different nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Producing hybrid nucleic acids, useful for expressing novel therapeutic polypeptides, by mixing the same or different nucleic acids having one or more recombination sites in the presence of recombination proteins,
                                                                                                                                                                                                                                 Bacteriophage lambda; recombination; att site; PCR primer; lambda Int;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 25; DB 22; Length 25; 100.0%; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Byrd DRN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Temple GF, Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Prec. ...
25
                                                                                                                                                                                                   Phage-lambda recombination site attR1.
                             GricaGCriririciacaaacrigi 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure, Fig 24A; 357pp; English.
                                                                                                                                                                                                                                                 lambda integrase; therapeutic; ss.
                                                                                                                                                                                                                                                                                                                                                                                                     10-DEC-1999; 99US-0169983.
09-MAR-2000; 2000US-0188020.
                                                                                                                                                                                                                                                                                                                                                                      11-DEC-2000; 2000WO-US33546
                                                                                                        AAS06181 standard; DNA; 25
                                                                                                                                                                    12-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                              Bacteriophage lambda
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHEO D.
BRASCH M A.
TEMPLE G F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HARTLEY J L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brasch MA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-356174/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BYRD D R N.
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Best Local Similarity
Matches 25; Conser
                                                                                                                                                                                                                                                                                                            WO200142509-A1
                                                                                                                                                                                                                                                                                                                                           14-JUN-2001
                                                                                                                                     AAS06181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHEO/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TEMP/)
(HART/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BYRD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cheo D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          e.g.
                                                                           RESULT 4
                                                                                         AAS06183
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The present invention relates to a method for in vitro cloning of a nucleic acid of interest. The method involves mixing in vitro two vectors each comprising at least one recombination site and the nucleic acid of interest; incubating the mixture in the presence of at least one recombination protein to result in recombination of the recombination sites, leading to production of a chimeric nucleic acid molecule comprising the nucleic acid of interest; contacting hosts with the mixture, and selecting for a host comprising the vectors comprising the second vectors comprising the second vectors comprising the second vectors comprising the second vectors comprising the recombinantion site, which may be used in the method of the present
                                                                                                                                                                                                                                                                                                                                                                                   In vitro cloning of nucleic acid involves mixing vectors comprising recombination sites and/or nucleic acid, incubating mixture to produce chimeric molecule, contacting hosts with mixture and selecting host -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli core region recombinant site attR1 SEQ ID NO:9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 25; DB 22; Length 25; 100.0%; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Core region, recombination site, cloning, chimeric DNA, characteristic, mutation, att site, lox site, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gricagcriririgiacaaacrigi 25
                                                                                                                 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 25; Column 46; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GTTCAGCTTTTTTGTACAAACTTGT
                                                                                                             Recombination site; cloning; att;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
 BP.
                                                                                                                                                                                                                                                                                                    TECHNOLOGIES INC.
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                                                                                                                                                                                                                               98US-0005476
                                                                                                                                                                                                                                                          96US-0663002.
95US-0486139.
AAF55743 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAC87874 standard; DNA; 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                       (first entry)
                                                                                   Recombination site attR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                              Brasch MA;
                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-136877/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia coli.
                                                                                                                                                                                                                                                                                                 (LIFE-) LIFE
                                                                                                                                         Unidentified
                                                                                                                                                                      JS6171861-B1
                                                                                                                                                                                                                             12-JAN-1998;
                                                                                                                                                                                                                                                          07-JUN-1996;
                                                                                                                                                                                                                                                                       07-JUN-1995;
                                                                                                                                                                                                                                                                                                                             Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Core region;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-MAR-2001
                                                       12-APR-2001
                                                                                                                                                                                                 09-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nvention
                            AAF55743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAC87874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 8
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Conservative

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RESULT 5

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have the desired characteristics and/or nucleic acid segments. The methods can also be used for changing vectors. The oligonucleotides AAX78935-X78994 are used in the method of the invention.

BP; 5 A; 4 C; 4 G; 12 T; 0 other;

Sequence 25

888888

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Gaps

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100.0%; Score 25; DB 20; Length 25; 100.0%; Pred. No. 0.32;

Pred. No. 0.3 Mismatches 25

100.08; FL

Conservative

Best Local Similarity Matches 25; Conser

Query Match

1 GTTCAGCTTTTTTGTACAAACTTGT

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                                                                    AAT48210-25 are att recombination site core region DNA sequences. The cree region has at least one engineered mutation that enhances recombination in vitro in the formation of a Cointegrate or Product DNA. These core regions can be incorporated into novel vector donc DNA molecules. The nucleic acids, vectors and methods of the invention are used to obtain chimeric nucleic acid using recombination proteins and engineered recombination sites in vitro or in vivo. The improved specificity, speed and yields of the invention facilitates DNA or RNA subcloning, regulation or exchange useful for any related purpose, e.g. in vitro recombination of DNA segments, and in vitro or in vivo insertion or modification of transcribed, replicated, isolated or genomic DNA or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to novel methods for cloning or subcloning one or more nucleic acid molecules (NAMS) comprising: (a) combining in vitro or in vivo: (1) at least one insert donor molecules (IDMS) comprising one or more desired nucleic acid segments flanked by at least 2 recombination sites which do not recombine with each other; (2) one or more vector donor molecules (VDMS) comprising at least 2 recombination sites which do not recombine with each other; and (3) one or sites which do not recombine with each other; and (3) one or more site-specific recombination porteins; (b) incubating the combination to transfer one or more of the desired segments into one or more of the WDMs, thereby producing one or more desired product molecules (PMS). The methods can be used for the efficient and specific recombination of NAM segments. They can be used to generate chimeric DNA or RNA molecules that
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 25; DB 18; Length 25; 100.0%; Pred. No. 0.32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cloning; donor; recombination site; vector; chimeric; ss.
                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oligonucleotide #9 for recombination and cloning method.
                                                                                                                                                                                                                                                                                                                           Sequence 25 BP; 5 A; 4 C; 4 G; 12 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Temple GF;
                                                                                                                                                                                                                                                                                                                                                                                                 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GITCAGCITITIGIACAACTIGI 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GTTCAGCTTTTTTGTACAAACTTGT 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 161; 185pp; English.
                                    Claim 14; Page 55; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hartley JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New nucleic acid cloning methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAX78943 standard; DNA; 25 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LIFE-) LIFE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100.0%;
es 25; Conservative (
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97US-0065930.
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vitro or in vivo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        a gene/partial gene, using recombinatorial cloning by incubating the nucleic acids in the presence of a recombination protein under conditions for recombination -
                                                                                                                                                                                                                           Recombination site; copy number; replicon; recombinatorial cloning;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methods for apposing nucleic acids comprising an expression signal
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   GITCAGCITITITGIACAACTIGI
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useful for recombination cloning.
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95US-0486139.
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                                                                                      AAD14437 standard; DNA; 25
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                                                                                                                                                                                                                                                                            Unidentified
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                                                  RESULT 3
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Att site nucleotid Artificial plant c Plasmid pEGC701 c Oligonucleotide MO att site PCR prime PCR primer attRl u Destination vector

ABZ58734 ABT16628 AAH19591 ABL58593

AAC55545 AAS06217

AAC55503

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AAC55458

Destination vector GST expression cas

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 November 6, 2003, 21:05:38; Search time 111.5 Seconds (without alignments) 605.255 Million cell updates/sec
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2: /SIDSI/Gcgdata/geneseq/geneseqn-embl/NA1981.DAT:*

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29: /SIDSI/Gcgdata/geneseq/geneseqn-embl/NA2000.DAT:*

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          GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                                                                                                                      2552756 seqs, 1349719017 residues
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Listing first 45 summaries
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25
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19 SUMMARIES

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Result		Query	Query			
No.	Score		Length	DB	TD CI	Description
	25	100.0	25	18	•	attR1 core region.
73	25	100.0	25	20	AAX78943	Oligonucleotide #9
m	25	100.0	25	22	AAD14437	Recombination site
4	25	100.0	25	22	AAS06181	Phage-lambda recom
Ŋ	25	100.0	25	22	AAF55743	Recombination site
9	25	100.0	25	22	AAC87874	Escherichia coli c
7	25	100.0	25	24	AB082121	Core seguence of r
œ	25	100.0	25	25	ACC44658	Recombination site

Nucleic acids, vectors and methods to obtain chimeric nucleic acid - using recombinant proteins and engineered recombination sites in

(LIFE-) LIFE TECHNOLOGIES INC

Brasch MA, Hartley JL; WPI; 1997-065168/06.

	ALIGNMENTS		
ir 1 3218 AAT48218 stand	T 1 218 AAT48218 standard, DNA, 25 BP.		
AAT48218;			
20-OCT-1997 (	(first entry)		
attR1 core region.	ion.		
att recombinat vector; subclo	att recombination site; core region; mutation; enhance; recombina vector; subcloning; regulation; exchange; ss.	enhance;	recombina
Synthetic.			
WO9640724-A1.			
19-DEC-1996.			
07-JUN-1996;	96WO-US10082.		
07-JUN-1995;	95US-0486139.		

tion;

TITLE Recombinational cloning using engineered recombination sites JOURNAL Patent: US 6171861-A 16 09-JAN-2001;
FEATURES Location/Qualifiers source 1.0.25
/organism="unknown"
5 a 4 c 6 g 10 t

BASE COUNT ORIGIN

0; Gaps Query Match

83.2%; Score 20.8; DB 6; Length 25;
Best Local Similarity 91.7%; Pred. No. 4.3e+02;
Matches 22; Conservative 0; Mismatches 2; Indels

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Search completed: November 6, 2003, 23:06:41 Job time : 603 sec8

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AR124536
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AR124531
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TITLE
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                                                                                                                                                                                                                                                                                                                                                           During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations where differences are found these are annotated as variations together with a note of the overlapping clone amen. Note that the variation annotation may not be found in the sequence submission contresponding to the overlapping clone, as we submit sequences with monly a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Emt., EMBL; Swi, SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C elegans/wormpep Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Inther information see http://www/Projects/D_rerio/fishmask.shtml CHT1-27FBL; if from a CHORI-211 BAC library
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                                                                                                           Giselle,H.

Direct Submission
Submitseion
Submitseo (12-DEC-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zface@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Dec 16, 2002 this sequence version replaced gi:24940082.
               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
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Recombinational cloning using nucleic acids having recombination
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26034 c 25755 g 45614 t
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0; Mismatches
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Pred. No. 32
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Web site: http://www.sanger.ac.uk
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/db_xref="taxon:7955"
/clone="CH211-237E12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Danio rerio"
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                                                                                                                                                                                                                                                                                                                                    Contact: zface@sanger.ac.uk
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JP 2002500861-A/43.
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Best Local Similarity 92.0%;
Matches 23; Conservative C
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BD131369
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Hartley, J.L., Brasch, M.A., Temple, G.F. and Fox, D.K.
Recombinational cloning using nucleic acids having recombination
Patent: JP 2002500861-A 43 15-JAN-2002;
LIFE TECHNOLOGIES INC
                                 Gaps
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Harrley, J.L. and Brasch, M.A.
Recombinational cloning using engineered recombination sites
Patent: 18 6171861-A 11 09-JAN-2001;
Location/Qualifiers
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                                                                                                                                                                                              /organism='Unknown'.
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Pred. No. 2.9e+02;
3; Mismatches 1;
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Sequence 11 from patent US 6171861.
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Sequence 16 from patent US 6171861.
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1 (bases 1 to 25)
Hartley, J.L. and Brasch, M.A.
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91.7%;
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Best Local Similarity 83.3%;
Matches 20; Conservative 3
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PAT 21-NOV-2002
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Pred. No. 1.4e+02;
0; Mismatches 2; Indels
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                   linear
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Pred. No. 1.46+02;
0; Mismatches 2;
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Patent: WO 02066622-A 54 29-AUG-2002;
Novozymes A/S (DK)
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Lipolytic enzyme genes
Patent: WO 02066622-A 27 29-AUG-2002;
Novozymes A/S (DK)
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                AX525429 51 bp 1
Seguence 27 from Patent W002066622.
AX525429
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Best Local Similarity 92.0
Matches 23; Conservative
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Best Local Similarity
Matches 23; Conservat
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AX525456/c
LOCUS
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AX525429/c
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AL935194
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87.2%; Score 21.8; DB 6; Length 51;
Best Local Similarity 92.0%; Pred. No. 1.4e+02;
Matches 23; Conservative 0; Mismatches 2; Indels
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Pred. No. 1.4e+62;
0; Mismatches 2; Indels
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Lipolytic erzyme genes
Patent: WO 02066622-A 11 29-AUG-2002;
Novozymes A/S (DK)
Location/Qualifiers
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Sequence 19 from Patent WO02066622.
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              GTTCAGCTTTTTTGTACAAACTTGT 25
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AX525421.1 GI:25170307
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Best Local Similarity 92.0%;
Matches 23; Conservative C
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AX25413/c
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SOURCE
ORGANISM
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DEFINITION ACCESSION VERSION

REFERENCE AUTHORS TITLE JOURNAL

FEATURES

AX525421/c LOCUS

RESULT 34

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REFERENCE AUTHORS TITLE JOURNAL

FEATURES

BASE COUNT ORIGIN

BASE COUNT ORIGIN

RESULT 35

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Danio rerio (zebrafish)

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5 c 4 g 10 t 1 others
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/function="35S promoter"
14660. 16258
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/note="pyruvate orthophosphate dikinase (pdk)"
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MAYO FOUNDATION FOR MEDICAL EDUCATION AND RESEARCH (US)
Location/Qualifiers
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Pred. No. 1.6e+02;
0; Mismatches 2; Indels
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Pred. No. 26;
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Sequence 7 from Patent WO0174861.
AX269136
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                  terminator"
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                                                  /note="left border"
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95.8%; Pred
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'gene="spec"
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Best Local Similarity 92.0
Matches 23; Conservative
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/note="pHELLSGATE is a derivative of cloning vector
pART27"
                                                                  2 (bases 1 to 18691)
Waterhouse,P.M.
Direct Submission
Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'note="neomycin phosphotransferase II (nptII)"
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265. .448
silencing in plants
Plant J. 27 (6), 581-590 (2001)
21461301
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Gaps

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Gaps

us-10-055-001a-4.rge

TITLE

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kanomycin resistance protein; neomycin phosphotransferase II; nptII
gene; promoter; speC gene; spectinomycin resistance protein;
transposon Tn7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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/af21 c 4607 g 4626 t
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transl_table=11

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Cloning vector pHELLSGATE
artificial sequences; vectors.
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Cloning vector pHELLSGATE.
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Construct design for efficient, effective and high-throughput gene silending in plants
Plant J. 27 (6), 581-590 (2001)
kanowycin resistance protein; neomycin phosphotransferase II; nptII gene; promoter; speC gene; spectinomycin resistance protein; transposon Tn7.
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pART27"
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Direct Submission
Submitted (A-MAY-2001) Materhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
Location/Qualifiers
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265. .448
                                                                                                           artificial sequences; vectors.
                                                                 Cloning vector PHELLSGATE Cloning vector PHELLSGATE
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RESULT 26 AR163186 LOCUS ACCESSION VERSION KEYWORDS

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I (bases 1 to 25)

Is Hartley, L., Brasch, M.A., Temple, G.F. and Fox, D.K.

Recombinational cloning using nucleic acids having recombination

I Extent: JP 2002500861-A 15 15-JAN-2002;

LIFE TECHNOLOGIES INC

OS Unknown

PD 15-JAN-2002

PP 26-OCT-1998 JP 200518069

PR 24-OCT-1999 JP 200550861-A/15

PR 24-OCT-1997 MCHAEL A BRASCH, GARX F TEMPLE, DONNA K FOX PC

CLEN'15/09.CL2Q1/68, CL2N15/00

CC Description of Unknown Organism: recombination products FH

Key Location/Qualifiers
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Recombinational cloning using nucleic acids having recombination
                              Hartley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: BF 1229113-A 15 07-AUG-2002;
INVIRROGEN CORPORATION (US)
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/organism="unidentified"
/mol_type="genomic DNA"
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Harrley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: US 6270969-A.15 07-AUG-2001;
Location/Qualifiers
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/wol_type="genomic DNA"
/db_rsef="taxon:32644"
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1 (bases 1 to 25)
Hartley, J. L., Brasch, M.A., Temple, G.F. and Fox, D.K.
Recombinational cloning using nucleic acids having recombination patent: JP 2002500861-A 10 15-JAN-2002;
LIFE TECHNOLOGIES INC
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PD 15-JAN-2002
PD 15-JAN-2002
PP 26-OCT-1998 JP 2000518069
PR 24-OCT-1997 US 60/065830,23-OCT-1998 US 09/177387 PI
AMER L HARTLEY, MICHAEL A BRASCH, GARY F TEMPLE, DONNA K FOX PC
C12N15/09,C12Q1/69,C12N15/00
CC Description of Unknown Organism: recombination products FH
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BD131368 25 bp DNA linear PAT 18-SEP-2002
Recombinational cloning using nucleic acids having recombination
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Hartley,J.L., Brasch,M.A., Temple,G.F. and Fox,D.K.
Recombinational cloning using nucleic acids having recombination
Patent: JP 2002500861-A 42 15-JAN-2002;
                                                                                                                                                                                                                                                 OS Unknown

OS Unknown

PN JP 2002500861-A/42

PD 15-JAN-202

PF 26-OCT-1997 US 60/065930,23-OCT-1998 US 09/177387 PI

JAMES L HARTLEY, MICHAEL A BRASCH, GARX F TEMPLE, DONNA K FOX PC

C12N15/09, C12Q1/68,012N15/00

CC Description of Unknown Organism: recombination products FH

Key

Location/Qualifiers

FT source 1...25

FT formulation products FH

Cyganism='Unknown'.
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Hattley,J.L. and Brasch,M.A.
Recombinational cloning using engineered recombination sites
Patent: 18 6171861-A 15 09-JAN-2001;
Location/Qualifiers
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76.0%; Pred. No. /z,
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Sequence 15 from patent US 6171861.
AR124535
AR124535.1 GI:14109896
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Pred. No. 90;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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JP 2002500861-A/42.
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/product="gyzase target toxin"
/product="gyzase target toxin"
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/translation="MQFKVYTYKRESKYRLFVDVQSDIIDTPGRRWYIPLASARLLSD
/translation="MQFKVYTYKRESKYRLFVDVQSDIIDTPGRRWYIPLASARLLSD
/mote="attR2; Gateway; Bacteriophage Lambda recombination
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SSLMSBYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPWVSFTSFDLNV
ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDBWQGG
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/note="his-3 right flank; his-3 target integration site"
3549 c 3559 g 3497 t
Construction of Neurospora crassa Histidine-3 (his-3)-Gene Replacement Plasmids
Unpublished
2 (bases 1 to 13990)
Haag,J.R., Lee,D.W. and Aramayo,R.
Direct Submission
Submitted (27-AUG-2002) Biology, Texas A&M University, BSBW #415,
College Station, TX 77943-3258, USA
Location,Qualifiers
1. 13990
                                                                                                                                                                                                                                                                            note="his-3 left flank; his-3 target integration site"
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Hartley, J. . and Brasch, M.A.
Recombinational Cloning using engineered recombination sites
Patent: US 6171861-A 10 09-JAN-2001;
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/specific_host="Neurospora crassa"
/db_xref="taxon:211505"
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Sequence 10 from patent US 6171861.
AR124530
AR124530.1 GI:14109891
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ACCESSION
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KEYWORDS
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AUTHORS
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AR124530
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JOURNAL
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REFERENCE
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Recombinational clouing using engineered recombination sites
Patent: EP 1227147-A 10 31-UUL-2002;
INVITROGEN CORPORATION (US)
Location/Qualifiers
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DB 6;
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1 (bases 1 to 25)
Hartley, V.L. and Brasch, M.A.
Recombinational cloning using enginee
Patent: US 6270969-A 10 07-AUG-2001;
Location/Qualifiers
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Score 23.4; DE Pred. No. 34; 0; Mismatches
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                                                                                                                                                    Sequence 10 from patent US 6270969.
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1 Similarity 96.0%;
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                                                                              Goossens, A. and Inz, D.
The use of genes encoding membrane transporter pumps to stimulate the production of secondary metabolites in biological cells Patent: WO 02083888-A 9 24-OCT-2002;
Vlaams Interuniversitair Instituut voor Biotechnologie vzw. (BE)
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his-3 integration vector pJHAM007
artificial sequences; vectors.
1 (bases 1 to 13990.
Haag, J.R., Lee, D.W. and Aramayo, R.
bescription of a GATEWAY Destination Vector For High-Throughput
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Syngenta Participations AG (CH) ; Universitaet Zuerich (CH)
Location/Qualifiers
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/ 3271 c 3178 g 3482 t
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AX29cance 20 from Patent W00206490.
AX356862
AX356862.1 GI:18674110
                                                                                                                                                                                      1. 12789 / Organism="synthetic con/mol-type="genomic DNA" / Mol-type="dearonic DNA" / db & xref="taxon:3260" / note="vector pK7WG2D" a 3326 c 3397 g 301
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(bases 1 to 1267)

(riswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, E.P.

A toolkit for transformation and mutagenesis in Drosophila using piggyBac
                                                                                                                                                                                                                                                                                                                                                                                          Unpublished
2 (bases 1 to 12677)
2 (bases 1 to 12677)
3 (bases 2 to 12677)
6 riswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, E.P. Direct Submission
Submitted (13-256-22002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, N
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/note="Gateway recombination cassette B; attRl CmR ccdB
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1. .12677
/ Organism="piggyBac transformation vector pB-UGIR value" type="genomic DNA"
/ Mol Lype="taxon:221642"
complement(11. .>620)
/ txansposon="piggyBac transposable element"
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/note="5x UAS hsp70 TATA signal"
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piggyBac transformation vector pB-UGIR w+
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Sequence 9 from Patent WO02083888.
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/note="SV40"
5247. .9369
/gene="w"
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note="RpS5"
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piggyBac transformation vector pB-UGIR w+
artificial sequences; vectors.
1 (Seas 1 to 1267),
Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, B.P.
A toolkit for transformation and mutagenesis in Drosophila using
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Unpublished
2. (blases 1 to 12677)
Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spai
Direct Submission
Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
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7. organism="piggyBac transformation vector pB-UGIR

/mol type="genomic DNA"

/db_xref="taxon:221642"
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7note="wmini-white; derived from Drosophila"
complement(<5370...9819)
7transposon="piggyBac transposable element"
7924 c 2833 g 3497 t
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/gene="w"
/note="min-white; derived from Drosophila"
complement(<7698. .8147)
/transposon="piggyBac transposable element"
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//note="Sx UAS hsp70 TATA signal"
1003. .2713
/note="Gateway recombination cassette
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/note="SV40"
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complement(11..>620)
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Thoses 1 to 11005)
Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, E.P. A toolkit for transformation and mutagenesis in Drosophila using
           2 (bases 1 to 11005)
Griswold,C.M., Roebuck,J., Andersen,R.O., Stam,L.F. and Spana,E.P.
Direct Submission
Submitted (13-DEC-2002) Invertebrate Targets, Syngenta
Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle Park, N
27709, USA
                                                                                                                                                           /organism="piggyBac transformation vector pB-UGateway w+"
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1003. 2713
/note="Gateway recombination cassette A; attR1 CmR ccdB
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Biotechnology, Inc., 3054 Cornwallis Rd, Research Triangle
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/gene="w"
/note="min-white, derived from Drosophila"
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/transposon="piggyBac transposable element"
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/note="5x UAS hsp70 TATA signal"
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                                                                                                                                                                                                                                                                                                                                           2726. .3040
/note="RpS5"
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/note="SV40"
                                                                                                                                                                                                                                                                                                                                                                              number=3
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Best Local Similarity
Matches 25; Conserv
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g à

Park, NC

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CmR

Spana, E.P.

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Another frame A"

1610. 1736

Inote="attR2 of Gateway conversion cassette frame A"

1762. 2048

Inote="contains intron 1 of Arabidopsis thaliana WRKY
transcription factor 33"

Complement(2073. 3783)

Inote="antisense orientation of Gateway conversion
cassette frame A containing attR1-R2 repeats, CMR gene and
ccdB gene"
ccmplement(2073. 2199)

Inote="attR2 of Gateway conversion cassette frame A"
complement(2073. 22946)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of DNA gyrase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /produĞt="CmR"

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SSLWSEYHDDFRQFHITYSQDVAQCYGENLAYFPKGFIENNFFVSANPWVSFTSFDLNV

ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="ccdB"
/note="encodes a cytotoxic protein that is a potent poison
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PiggyBac transformation vector pB-UGateway w+, complete sequence.
AY196824
                                                                    /protein_id="AAM62301.1"
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piggyBac transformation vector pB-UGateway w+
artificial sequences; vectors.
1 (bases 1 to 11005)
Griswold, C.M., Roebuck, J., Andersen, R.O., Stam, L.F. and Spana, B.P.
A toolkit for transformation and mutagenesis in Drosophila using
piggyBac
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/note="attRl of Gateway conversion cassette frame A"
a 2150 c 2185 g 2347 t
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100.0%; Pred. No. 2.4
:ive 0; Mismatches
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of DNA gyrase"
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THYVKNKHKFRFYAFHILLALLMNAHBFRAMANGBLVIMBSVHDCYTYFHEQTBTF
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ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDBWQGG
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1 (bases 1 to 9019)
Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.
pJawohl8-RNAi a binary vector for gene silencing in plants
Unpublished
2 (bases 1 to 9019)
Ulker, B., Lipka, V., Rademacher, T.R. and Somssich, I.E.
Direct Submission
Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
f. Zuechtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="binary plant gene silencing vector for one-step cloning of inverted sequences"
3803. 9019
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="sense orientation of Gateway conversion cassette frame A containing attRl-R2 repeats, CmR gene and ccdB gene"
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                         complement (1657. .3783)
/note="attRl of Gateway conversion cassette frame
1 2150 c 2185 g 2347 t
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                                                                                                                                    Length 9019;
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hote="attR1 of Gateway conversion cassette
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function="confers resistance to antibiotic
                                                                                                                                                                                    Indels
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/focus
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Binary vector pJawohl8-RNAi, complete sequence.
AF408413
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1 Similarity 100.0%; Score 25; DB 12;
25; Conservative 0; Mismatcher 0.
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db_xref="GI:21552737"
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Binary vector pJawohl8-RNAi
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1263. .1568
/gene="ccdB"
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Length 9019;

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/gene="ccdB"
/note="encodes a cytotoxic protein that is a potent poison
of DNA gyrase"
/codon_start=1
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KVSRELYPVVHIGDESWRMMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
complement (2888. .3547)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LKTVKKNRHKFYPAFIHILARLMNAHPBFRMAMKDGELVIMDSVHPCYTVFHEQTETF
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ANMDNFFAPVFTMGKYYTQGDKVLMPLAIQVHHAVCDGFHVGRMLNELQQYCDEWQGG
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KVSRELYPVVHIGDESWRMMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
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'db_xref="GI:21552737"
'translation="MEKKITGYTTVDISQWHRKEHFEAFQSVAQCTYNQTVQLDITAF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="encodes a cytotoxic protein that is a potent poison of DNA gyrase"
                                                                                                                conversion cassette
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                                                                                                                                                                                               26. .152
/note="attR1 of Gateway conversion cassette frame A"
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complement(2073. .2199)

hote="attR2 of Gateway conversion cassette frame complement(2241. .2546)
/gene="ccdB"
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/function="confers resistance to antibiotic
                                                                                                                                                                                                                                                                                                                                                         function="confers resistance to antibiotic
     pJawohl3-RNAi"
                                                                                       26.<sup>7</sup>.1733
/note="sense orientation of Gateway c
frame A containing attR1-R2 repeats,
/organism="Binary vector
/mol_type="genomic DNA"
/db_xref="taxon:176105"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /protein_id="AAM62301.1"
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/protein_id="AAM62303.1"
/db_xref="G1:21552740"
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/codon start=1
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1263. 15
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/gene="ccdB"
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/gene="CmR"
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/gene="CmR"
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1 (bases 1 to 9019)
2 birect Submission
3 birect Submission
5 Submitted (08-AUG-2001) Biochemistry, Max-Planck-Institut
6 Lacchtungsforschung, Carl-von-Linne Weg 10, Koeln, NRW D-50829,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="binary plant gene silencing vector for one-step
cloning of inverted sequences"
3803. .9019
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Binary vector pJawohl8-RNA1, complete sequence.
AF408413
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Pred. No. 2.7;
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                                                                                                                                                                                                                                                                                                                                                            DNA
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Pred. No. 2.6;
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Patent: WO 0188121-A 10 22-NOV-2001;
Devgen NV (BE)
                                                                                                                0; Mismatches
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/organism="synthetic const
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                                                                                                                                                                                                                                                                                                                                                 Sequence 10 from Patent W00188121.
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Matches 25; Conservative
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Jakoby,M.J., Heim,M.A. and Weisshaar,B.
Use of a gateway compatible vector for transient plant transfection
Unpublished
2 (bases 1 to 4462)
Jakoby,M.J.
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IBLDINSGKILESFRPERFFPMGFFKVLLCGAVLSRIDAGGEQLGRRIHYSQNDLVE
YSPVTEKHLTDGMTVRELCSAAITMSDNTAANLLITIGGFKELTAFLHNMGDHVTRL
DRWEPELNEAIPNGESTTMPVAAMTTLRKLITGELLTAGROQLIDWMEADKYAGFL
LRSALPAGWPIADKSGAGERGSRGIIAALGPDGKPSRIVVIYTTGSQATMDERNRQIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="chloramphenicol acetyl transferase"
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SSLWSEYHDDFRQFLHIYSQDVACYGENLAYFPKGFIENMFFVSANPWVSFTSFDLNV
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KVSRELYPVVHIGDESWRMMTTDMASVPVSVIGEEVADLSHRENDIKNAINLMFWGI"
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     circular SYN 27-MAR-2003
                                                                                                                                                                                                                                                              Direct Submission
Submitted (26-MAR-2003) Jakoby M.J., Salamini, MPI for Plant
Breeding Research, Carl-von-Linne Weg 10, 50829 Koeln, GERMANY
Location/Qualifiers
                                                  AJ551314.1 GI:29335742
amp gene; beta lactamase; cat gene; ccdB gene; chloramphenicol
acetyl transferase; control of cell death B protein.
Transfection vector pBrdest
Transfection vector pBrdest
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product="control of cell death B protein"
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/mol_type="genomic DNA"
/db_xref="taxon:225975"
/note="35S"
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db xref="GI:29335745"
Transfection vector pBTdest.
                                                                                                                                             artificial sequences; vectors.
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/gene="cat"
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/note="358"
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/note="attR1"
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/note="attR2"
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/gene="ccdB"
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/gene="ccdB"
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                                                                                                                                                                                                                 Escherichia coli
Seberichia coli
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Escherichia.
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Modulation of secondary metabolite production by zinc binuclear
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/organism="synthetic construct"
/mol_type="genomic DNA"
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db_xref="taxon:44 g 504 t
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Patent: WO 02066653-A 63 29-AUG-2002;
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Patent: WO 0224865-A 9 28-MAR-2002;
Microbia, INC. (US)
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BD131335 25 bp DNA linear PAT 18-SEP-2002
Recombinational cloning using nucleic acids having recombination
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Recombinational coloning using engineered recombination sites
Patent: EP 1227147A 9 31-UUL-2002;
INVITROGEN CORPORATION (US)
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Hartley, J.L. and Brasch, M.A.
Recombinational cloning using engineered recombination sites
Patent: US 6270969-A.9 07-AUG-2001,
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	AR124529 Sequence AR431480 Sequence AX491648 Sequence AX491649 Sequence BD131335 Sequence BD131335 Sequence AX703501 Sequence AX703501 Sequence AX703501 Sequence AX7035037 Sequence AR408413 Binary ve AR408413 Binary ve AR408413 Binary ve AR408413 Binary ve AX196824 PiggyBac AX196824 PiggyBac	AX196625 FiggyBac AX196625 FiggyBac AX35662 Sequence AX356662 Sequence AX124530 Sequence AR124530 Sequence AX491649 Sequence AX491649 Sequence AX491649 Sequence AX491650 Sequence AX491650 Sequence AX491650 Sequence AX491650 Sequence AX491650 Sequence AX491650 Sequence AX41653186 Recombina AR124535 Sequence AR16435 Sequence	AX491654 Sequence AX498625 Sequence BD131341 Recombina AJ311874 Cloning v AX269136 Sequence AX525413 Sequence AX525413 Sequence AX525426 Sequence AX525429 Sequence AX525429 Sequence AX525429 Sequence AX525430 Sequence AX525430 Sequence AX124531 Sequence AX124531 Sequence AX163187 Sequence AX163187 Sequence AX163187 Sequence AX491650 Sequence AX491650 Sequence	linear PAT 16-MAY-2001
SUMMARIES	AR124529 AR163180 AA491648 AA491648 BD131335 AX684690 AX703501 AX703501 AX306327 AF408413 AY396824 AX196824	AY196825 AX196825 AX590202 AX366862 AX1641339 AR144530 AR163181 AX491649 BD13136 BD13136 AR114435 AR114435	AX491654 AX498625 BX498625 BX1313134 CVE311874 CVE311874 AX526413 AX526421 AX526421 AX526421 AX526429 AX526429 AX526421 AX124536 AR124536 AR163182 AR163182 AX163182 AX491650 AX491656	ALIGNMENTS  25 bp DNA  1 GI:14109890 ied. 1 to 25) .L. and Brasch, M.ALional cloning using engineered is G171861-A 9 09-37AN-2001; Location/Qualifiers
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